```
   1 CGGTGCTGCC GGGCTCAGCC CCGTCTCCTC CTCTTGCTCC CTCGGCCGGG
  51 CGGCGGTGAC TGTGCACCGA CGTCGGCGCG GGCTGCACCG CCGCGTCCGC
 101 CCGCCCGCCA GCATGGCCAC CACCGCCACC TGCACCCGTT TCACCGACGA
 151 CTACCAGCTC TTCGAGGAGC TTGGCAAGGG TGCTTTCTCT GTGGTCCGCA
 201 GGTGTGTGAA GAAAACCTCC ACGCAGGAGT ACGCAGCAAA AATCATCAAT
 251 ACCAAGAAAT TGTCTGCCCG GGATCACCAG AAACTAGAAC GTGAGGCTCG
 301 GATATGTCGA CTTCTGAAAC ATCCAAACAT CGTGCGCCTC CATGACAGTA
 351 TTTCTGAAGA AGGGTTTCAC TACCTCGTGT TTGACCTTGT TACCGGCGGG
 401 GAGCTGTTTG AAGACATTGT GGCCAGAGAG TACTACAGTG AAGCAGATGC
 451 CAGCCACTGT ATACATCAGA TTCTGGAGAG TGTTAACCAC ATCCACCAGC
 501 ATGACATCGT CCACAGGGAC CTGAAGCCTG AGAACCTGCT GCTGGCGAGT
 551 AAATGCAAGG GTGCCGCCGT CAAGCTGGCT GATTTTGGCC TAGCCATCGA
 601 AGTACAGGGA GAGCAGCAGG CTTGGTTTGG TTTTGCTGGC ACCCCAGGTT
 651 ACTTGTCCCC TGAGGTCTTG AGGAAAGATC CCTATGGAAA ACCTGTGGAT
 701 ATCTGGGCCT GCGGGGTCAT CCTGTATATC CTCCTGGTGG GCTATCCTCC
 751 CTTCTGGGAT GAGGATCAGC ACAAGCTGTA TCAGCAGATC AAGGCTGGAG
 801 CCTATGATTT CCCATCACCA GAATGGGACA CGGTAACTCC TGAAGCCAAG
 851 AACTTGATCA ACCAGATGCT GACCATAAAC CCAGCAAAGC GCATCACGGC
 901 TGACCAGGCT CTCAAGCACC CGTGGGTCTG TCAACGATCC ACGGTGGCAT
 951 CCATGATGCA TCGTCAGGAG ACTGTGGAGT GTTTGCGCAA GTTCAATGCC
1001 CGGAGAAAAC TGAAGGGTGC CATCCTCACG ACCATGCTTG TCTCCAGGAA
1051 CTTCTCAGTT GGCAGGCAGA GCTCCGCCCC CGCCTCGCCT GCCGCGAGCG
1101 CCGCCGGCCT GGCCGGGCAA GCTGCCAAAA GCCTATTGAA CAAGAAGTCG
1151 GATGGCGGTG TCAAGAAAAG GAAGTCGAGT TCCAGCGTGC ACCTAATGGA
1201 GCCACAAACC ACTGTGGTAC ACAACGCTAC AGATGGGATC AAGGGCTCCA
1251 CAGAGAGCTG CAACACCACC ACAGAAGATG AGGACCTCAA AGCTGCCCCG
1301 CTCCGCACTG GGAATGGCAG CTCGGTGCCT GAAGGACGGA GCTCCCGGGA
1351 CAGAACAGCC CCCTCTGCAG GCATGCAGCC CCAGCCTTCT CTCTGCTCCT
1401 CAGCCATGCG AAAACAGGAG ATCATTAAGA TTACAGAACA GCTGATTGAA
1451 GCCATCAACA ATGGGGACTT TGAGGCCTAC ACGAAGATTT GTGATCCAGG
1501 CCTCACTTCC TTTGAGCCTG AGGCCCTTGG TAACCTCGTG GAGGGGATGG
1551 ATTTCCATAA GTTTTACTTT GAGAATCTCC TGTCCAAGAA CAGCAAGCCT
1601 ATCCATACCA CCATCCTAAA CCCACACGTC CACGTGATTG GGGAGGACGC
1651 AGCGTGCATC GCCTACATCC GCCTCACCCA GTACATCGAC GGGCAGGGTC
1701 GGCCTCGCAC CAGCCAGTCA GAAGAGACCC GGGTCTGGCA CCGTCGGGAT
1751 GGCAAGTGGC TCAATGTCCA CTATCACTGC TCAGGGGCCC CTGCCGCACC
1801 GCTGCAGTGA GCTCAGCCAC AGGGGCTTTA GGAGATTCCA GCCGGAGGTC
1851 CAACCTTCGC AGCCAGTGGC TCTGGAGGGC CTGAGTGACA GCGGCAGTCC
1901 TGTTTGTTTG AGGTTTAAAA CAATTCAATT ACAAAGCGG CAGCAGCCAA
1951 TGCACGCCCC TGCATGCAGC CCTCCCGCCC GCCCTTCGTG TCTGTCTCTG
2001 CTGTACCGAG GTGTTTTTTA CATTTAAGAA AAAAAAAAA AAAAAAAAA
2051 AAAAAAAAA A  (SEQ ID NO:1)
```

FEATURES:
5'UTR: 1-112
Start Codon: 113
Stop Codon: 1808
3'UTR: 1811

Homologous proteins:
Top 10 BLAST Hits

	Score	E
CRA|88000001156376 /altid=gi|7434378 /def=pir||JC5636 Ca2+/calm...	1083	0.0
CRA|18000004937293 /altid=gi|125289 /def=sp|P11730|KCCG_RAT CAL...	1066	0.0
CRA|18000005054755 /altid=gi|1657464 /def=gb|AAC48714.1| (U7297...	1038	0.0
CRA|105000014644765 /altid=gi|10443740 /def=gb|AAG17558.1|AF233...	994	0.0
CRA|105000014644764 /altid=gi|10443738 /def=gb|AAG17557.1|AF233...	989	0.0
CRA|18000004903800 /altid=gi|422770 /def=pir||A46619 Ca2+/calmo...	986	0.0
CRA|18000005152785 /altid=gi|3241847 /def=dbj|BAA28869.1| (D149...	986	0.0
CRA|18000004937876 /altid=gi|631810 /def=pir||S43845 Ca2+/calmo...	985	0.0
CRA|18000004937877 /altid=gi|560653 /def=gb|AAB30671.1| (S71571...	984	0.0
CRA|105000014644762 /altid=gi|10443734 /def=gb|AAG17555.1|AF233...	976	0.0

FIGURE 1A

BLAST dbEST Hits:

	Score	E
gi|12893350 /dataset=dbest /taxon=960...	1778	0.0
gi|12790010 /dataset=dbest /taxon=960...	1463	0.0
gi|10142161 /dataset=dbest /taxon=96...	1443	0.0
gi|10158540 /dataset=dbest /taxon=96...	1366	0.0
gi|12796371 /dataset=dbest /taxon=960...	1356	0.0
gi|12340179 /dataset=dbest /taxon=96...	1320	0.0
gi|9342125 /dataset=dbest /taxon=960...	1185	0.0
gi|12386814 /dataset=dbest /taxon=96...	1180	0.0
gi|12421686 /dataset=dbest /taxon=96...	1172	0.0
gi|12886387 /dataset=dbest /taxon=960...	1063	0.0

EXPRESSION INFORMATION FOR MODULATORY USE:
library source (from BLAST dbEST hits):
gi|12893350 Placenta
gi|12790010 breast
gi|10142161 Skin melanotic melanoma
gi|10158540 Ovary adenocarcinoma cell line
gi|12796371 breast
gi|12340179 Uterus leiomyosarcoma
gi|9342125 Lymph Burkitt's lymphoma
gi|12386814 Small Interstine duodenal adenocarcinoma
gi|12421686 Breast mammary adenocarcinoma
gi|12886387 placenta

Tissue Expression:
Human fetal whole brain

FIGURE 1B

```
  1 MATTATCIRF TDDYQLFEEL GKGAFSVVRR CVKKTSTQEY AAKIINTKKL
 51 SARDHQKLER EARICRLLKH PNIVRLHDSI SEEGFHYLVF DLVTGGELFE
101 DIVAREYYSE ADASHCIHQI LESVNHIHQH DIVHRDLKPE NLLLASKCKG
151 AAVKLADFGL AIEVQGEQQA WFGFAGTPGY LSPEVLRKDP YGKPVDIWAC
201 GVILYILLVG YPPFWDEDQH KLYQQIKAGA YDFPSPEWDT VTPEAKNLIN
251 QMLTINPAKR ITADQALKHP WVCQRSTVAS MMHRQETVEC LRKFNARRKL
301 KGAILTIMLV SRNFSVGRQS SAPASPAASA AGLAGQAAKS LLNKKSDGGV
351 KKRKSSSSVH LMEPQTTVVH NATDGIKGST ESCNTTTEDE DLKAAPLRTG
401 NGSSVPEGRS SRDRTAPSAG MQPQPSLCSS AMRKQEIIKI TEQLIEAINN
451 GDFEAYTKIC DPGLTSFEPE ALGNLVEGMD FHKFYFENLL SKNSKPIHTT
501 ILNPHVHVIG EDAACIAYIR LTQYIDGQGR PRTSQSEETR VWHRRDGKWL
551 NVHYHCSGAP AAPLQ  (SEQ ID NO:2)
```

FEATURES:
Functional domains and key regions:
[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
N-glycosylation site

Number of matches: 4

1	313-316	NFSV	(residues 313-316 of SEQ ID NO:2)
2	371-374	NATD	(residues 371-374 of SEQ ID NO:2)
3	384-387	NTTT	(residues 384-387 of SEQ ID NO:2)
4	401-404	NGSS	(residues 401-404 of SEQ ID NO:2)

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 5

1	33-36	KKTS	(residues 33-36 of SEQ ID NO:2)
2	48-51	KKLS	(residues 48-51 of SEQ ID NO:2)
3	259-262	KRIT	(residues 259-262 of SEQ ID NO:2)
4	352-355	KRKS	(residues 352-355 of SEQ ID NO:2)
5	353-356	RKSS	(residues 353-356 of SEQ ID NO:2)

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
Protein kinase C phosphorylation site

Number of matches: 3

1	47-49	TKK	(residues ...)
2	51-53	SAR	
3	410-412	SSR	

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
Casein kinase II phosphorylation site

Number of matches: 12

1	36-39	STQE	(residues 36-39 of SEQ ID NO:2)
2	51-54	SARD	(residues 51-54 of SEQ ID NO:2)
3	79-82	SISE	(residues 79-82 of SEQ ID NO:2)
4	94-97	TGGE	(residues 94-97 of SEQ ID NO:2)
5	109-112	SEAD	(residues 109-112 of SEQ ID NO:2)
6	385-388	TTTE	(residues 385-388 of SEQ ID NO:2)
7	386-389	TTED	(residues 386-389 of SEQ ID NO:2)
8	387-390	TEDE	(residues 387-390 of SEQ ID NO:2)
9	404-407	SVPE	(residues 404-407 of SEQ ID NO:2)
10	410-413	SSRD	(residues 410-413 of SEQ ID NO:2)
11	465-468	TSFE	(residues 465-468 of SEQ ID NO:2)
12	534-537	SQSE	(residues 534-537 of SEQ ID NO:2)

[5] PDOC00008 PS00008 MYRISTYL
N-myristoylation site

FIGURE 2A

Number of matches: 4

1	302-307	GAILTT	(residues 302-307 of SEQ ID NO:2)
2	375-380	GIKGST	(residues 375-380 of SEQ ID NO:2)
3	378-383	GSTESC	(residues 378-383 of SEQ ID NO:2)
4	400-405	GNGSSV	(residues 400-405 of SEQ ID NO:2)

[6] PDOC00100 PS00107 PROTEIN_KINASE_ATP
Protein kinases ATP-binding region signature

     20-43 LGKGAFSVVRRCVKKTSTQEYAAK   (residues 20-43 of SEQ ID NO:2)

[7] PDOC00100 PS00108 PROTEIN_KINASE_ST
Serine/Threonine protein kinases active-site signature

     132-144 IVHRDLKPENLLL   (residues 132-144 of SEQ ID NO:2)

[8] PDOC00364 PS00402 BPD_TRANSP_INN_MEMBR
Binding-protein-dependent transport systems inner membrane comp. sign

     405-433 VPEGRSSRDRTAPSAGMQPQPSLCSSAMR   (residues 405-433 of SEQ ID NO:2)

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	195	215	1.665	Certain
2	319	339	0.818	Putative

FIGURE 2B

BLAST Alignment to Top Hit:
>CRA|88000001156376 /altid=gi|7434378 /def=pir||JC5636
        Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123)
        II gamma-E - human /org=human /taxon=9606 /dataset=nraa
        /length=556
     Length = 556

 Score = 1083 bits (2771), Expect = 0.0
 Identities = 534/577 (92%), Positives = 539/577 (92%), Gaps = 12/577 (2%)
 Frame = +2

Query: 113 MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER 292
        MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER
Sbjct: 1   MATTATCTRFTDDYQLFEELGKGAFSVVRRCVKKTSTQEYAAKIINTKKLSARDHQKLER 60

Query: 293 EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI 472
        EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI
Sbjct: 61   EARICRLLKHPNIVRLHDSISEEGFHYLVFDLVTGGELFEDIVAREYYSEADASHCIHQI 120

Query: 473 IESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY 652
        IESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY
Sbjct: 121 IESVNHIHQHDIVHRDLKPENLLLASKCKGAAVKLADFGLAIEVQGEQQAWFGFAGTPGY 180

Query: 653 LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT 832
        LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT
Sbjct: 181 LSPEVLRKDPYGKPVDIWACGVILYILLVGYPPFWDEDQHKLYQQIKAGAYDFPSPEWDT 240

Query: 833 VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL 1012
        VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL
Sbjct: 241 VTPEAKNLINQMLTINPAKRITADQALKHPWVCQRSTVASMMHRQETVECLRKFNARRKL 300

Query: 1013 KGAILTTMLVSRNFSVGRQSSAPASPAASAAGLAGQAAKSLLNKKSDGGVKKRKSSSSVH 1192
        KGAILTTMLVSRNFS   AAKSLLNKKSDGGVK + ++ +
Sbjct: 301 KGAILTTMLVSRNFS--------------------AAKSLLNKKSDGGVKPQSNNKNSL 339

Query: 1193 L-----------MEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG 1336
        +   MEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG
Sbjct: 340 VSPAQEPAPLQTAMEPQTTVVHNATDGIKGSTESCNTTTEDEDLKAAPLRTGNGSSVPEG 399

Query: 1337 RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKTTEQLIEAINNGDFEAYTKICDPGLTSFE 1516
        RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKTTEQLIEAINNGDFEAYTKICDPGLTSFE
Sbjct: 400 RSSRDRTAPSAGMQPQPSLCSSAMRKQEIIKTTEQLIEAINNGDFEAYTKICDPGLTSFE 459

Query: 1517 PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ 1696
        PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ
Sbjct: 460 PEALGNLVEGMDFHKFYFENLLSKNSKPIHTTILNPHVHVIGEDAACIAYIRLTQYIDGQ 519

Query: 1697 GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ 1807   (SEQ ID NO:2)
        GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ
Sbjct: 520 GRPRTSQSEETRVWHRRDGKWLNVHYHCSGAPAAPLQ 556   (SEQ ID NO:4)

FIGURE 2C

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00069	Eukaryotic protein kinase domain	309.5	4.1e-89	1
CE00022	CE00022 MAGUK_subfamily_d	295.5	3.9e-87	1
CE00359	E00359 bone_morphogenetic_protein_receptor	14.8	0.0017	1
PF00534	Glycosyl transferases group 1	3.3	9.1	1
CE00031	CE00031 VEGFR	0.3	3.2	1
CE00292	CE00292 PTK_membrane_span	-59.7	1.5e-05	1
CE00287	CE00287 PTK_Eph_orphan_receptor	-63.5	0.00035	1
CE00291	CE00291 PTK_fgf_receptor	-90.9	0.0016	1
CE00286	E00286 PTK_EGF_receptor	-131.8	0.0056	1
CE00290	CE00290 PTK_Trk_family	-154.9	0.00012	1
CE00016	CE00016 GSK_glycogen_synthase_kinase	-180.4	1.2e-06	1

Parsed for domains:

Model	Domain	seq-f	seq-t		hmm-f	hmm-t		score	E-value
PF00534	1/1	31	65	..	161	195	.]	3.3	9.1
CE00031	1/1	133	161	..	1068	1093	..	0.3	3.2
CE00359	1/1	132	186	..	272	327	..	14.8	0.0017
CE00286	1/1	14	252	..	1	263	[]	-131.8	0.0056
CE00290	1/1	15	253	..	1	282	[]	-154.9	0.00012
CE00291	1/1	14	267	..	1	285	[]	-90.9	0.0016
CE00292	1/1	14	267	..	1	288	[]	-59.7	1.5e-05
CE00287	1/1	14	270	..	1	260	[]	-63.5	0.00035
PF00069	1/1	14	272	..	1	278	[]	309.5	4.1e-89
CE00022	1/1	10	305	..	13	316	..	295.5	3.9e-87
CE00016	1/1	1	345	[.	1	433	[]	-180.4	1.2e-06

FIGURE 2D

```
   1 TTGCCCCTGG CCTGGTCTCC CTGATCAACC CGCGCCTGAA GGGTTTCTTT
  51 CTAATAATGG CCCTGGTGCT TGCGCAAGTC TAGACTGTCA GCTCCCAGAG
 101 GGAAGGCGGC TGGCAGCTGG CTCTGCGCAG GCTGGGGGCG CCTCCCGGGC
 151 GTGCAGCCTG GCACAGGCTC CTTGACCTTG GCTCTCTCCC CACGTGCTAG
 201 GAGCCCGGTT GGGGGCTCGG GACCCGCGTG TAGGACCCGT CCAGAGAGGT
 251 CAGTGGTCCA GACTCCTACA CTCCTAACAC ATGCACCCTC GCATGCACGT
 301 TCCCGAGCCC GCGCGGGGTC CGCCCCGGGA CAAGCCCATA AGTCGCGAAC
 351 CTTCCAGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 601 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 651 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 901 NNNNNNNNNN NNNNNNNNNN NNNNNTGTAA GCCACCGGCG CCGGGCGGTC
 951 TCGACATTAA ATTTCAAAAT GTTTTCTCCG GTTTGTCACT TGTGGTTTTA
1001 CTATGTTCAA TGGGTCTCAC CAAGCAATTT TGCAAAATAG TTAACTTATT
1051 CTCTTTTTCT TACATGACTT CTTGACTTTG AGCCATAGTT AGGAAAGGTT
1101 TGCTCACTCT CACATTAGAG TAAAATTTAT CCACATTTTC ATCTAGGATT
1151 AGTGCTCATT TTTTTATTAT TATGAATATC TTCTTCATTT GGGGTTTGTT
1201 CATGTATATT CCATGAACAA TGGACGCGGG TGCAGCATTT TAGCATCAGC
1251 TATCCCCTTC CCATCCGCAA TGAGCTGGCC GCTGCAGCAG CCCCGGCCCC
1301 CCACCCCCAC CCGCGGCGCC GAGCCCGGCC ACTGCAGCCC CCGCCCCGCC
1351 CGCCCCCCCA GACGTTTCCA GAGCTCAGAG TGCGAGCTCC CGTTTGACGG
1401 GGACGTCAAG GAAAATAGCA TGGAAGGGG AGTTCTTGAT GTCTGACTGT
1451 GTCCTCTCTT CCCTTGCTGT CAGTTGAGCC GGGATGCAGT GAGATGAAAC
1501 CGGCTGTGGG GGGGTTTGAG CCTCACTTTG CCCCATGGTT GAGGGAGATT
1551 TCTCTTTCAG GGGATGGATAC CCTCTTTTTA ATCTTTCCTT CCCCGACCTT
1601 CAGCTGTTCC TGCTGAGAGA AGGGCAGGGT CTCTCTGCTC CCTTCTGCCC
1651 TGGTTCTCTT GGCCGGGACC GCAGGGCTGT CTGAGATGCA GCAGGTGTGT
1701 GTTTTCAGCA TCGCCCACCC GCTCCTGATG TGCAGCCTGA GGTGGAGGCT
1751 GTTGCCTTGC CCAGGGACTG GATGAGGGGG TGGGAGCGCG GCACGCCACC
1801 CACATCTGTT CAGTGTCCTG CGGTGGCCGC GTCCTTTTGC CTCATGTTGG
1851 ATGGTGGTGG TCACAGCGCC GGTGTGTGTG CATGTACGTG AGTGTGACTA
1901 GAGGTCTGGT GGTGGGAGCA TCATCGTCCC CAGACTTGAA GTGTGTCTGT
1951 GTCACTCTGC CCTGCTCCGT GTCCCAGTTC TTTTCCCCTT CTCCCTCCAG
2001 GGGTGCTTTC TCTGTGGTCC GCAGGTGTGT GAAGAAAACC TCCACGCAGG
2051 AGTACGCAGC AAAAATCATC AATACCAAGA AATTGTCTGC CGGGGGTGAG
2101 TGTTCCCTGT CTTGACCTCT TCCTGAGGGT GCCTCCAGGG GCCATGGTTT
2151 CTTTTGAGGA AGCCCCAGGA ATTGGGGGTT GTGCGTTTTA GCACTTGGAG
2201 AGGAGTTGGA ATTTCAGACT GGTTGGACTT TGTGTCAGGC TGAAGCCAGA
2251 AAAGGAGTTG CATGGGGGAC TGGAAGCGCC CAGGTACAAA AGAATGAAGG
2301 AAGAGATGCA AGTAGCTGCA GTGGCCCCCA AAGGCTCAAG GGAGTTCGGT
2351 CTTCAGGGAG GTGGAGGATA TGGGGGTAGT GGGTGGTACA GAATGGGGAG
2401 CTCTTAATTT GGGGCATTTG GAGCCTCTCC CTTTGGGGCA GTGGTGGCTA
2451 CTGCAGGCCT TTCCTGGTCC CTTCTTCACC ACGGGCTGAG TTAGGATGGA
2501 AATGCAGTAA GTGAGCAGCT CTGACAAAGC CAGCCTCCCC TGCCCACCAG
2551 GCGGCAGAAC AGACTCCCAA GGGAAGGGAA TCTGTAAACA TCAGGGGAGG
2601 CTGCTACTGG CGAGGGCTTC TCAGGAACAA ATTCTGCCAG ATGAACTTGA
2651 TTGCTTTTTT GATCAAATTA CAAAGTTGGT GGTGCAGCAG CAGATGTAGT
2701 CTGTCCTGGG TGGAGGGTGA TGCCTCATGG TCTAGAAATC CCAAAGGCCC
2751 GGTTTGGGCA GGAACTGCAC TGCCTCCGAA CTGCACTGCC TCCGAGTCTG
2801 AGGAGCATAA AGGCCAAGGC CTTGGGGCCT CACTTGCGAG ATCCTCCCAA
2851 GTACCTGAGG CTTGGAGGGT CAGGGCCTGT CTTTCACACC TTGAACCTAC
2901 ACTCTCTGAA CTTCCTATTG GGTACTTGCC AAACTCACCT CATCTGATAG
2951 GTGTAGACCC AGCAATGTGT GAAGTGCTCT GGGAACAGGT CTGGTGAGTA
3001 CAGAGGTCAG ATCTCGGAGG GCTGCAGGGT GCAGCTGGGG GACAAAGGTT
```

FIGURE 3A

```
3051 GTGAAACTCA GAGAAAGGAA TTAGGGCTGG GCAGTAGGAT GCCATAAATA
3101 TATTTGGAGC CAGGACACAT GCCCTGGGGA AGACATGGGC TTTGGCCAAT
3151 AATGACACGG GTTTCTCTGG GATAAGAGAC ATAATAGATG TCCCAAATGC
3201 TTAGAGAAGC TCTACAATTC CACGGGCTTC TGTCGTGTTG GCAGTTGTTC
3251 TGGGACCTGT TTAGCAGGGC CGTGTCCACT CCCTGACTGG GGACTCTCTC
3301 TCCATCCCTC TGGTAGGGCA CTAATTGCTG ACTCCCATCC AGCTCCATCT
3351 CTTGCTGTTC GTGTACATTG CCTATAAAGT TGGACTTGTT TGTTTTCTTT
3401 CTCTCTGGGT ACCTTGAGTC TGAGGATGGT TGCCATAGAG ATATGTGGGC
3451 AGTCAGATAC CCTGGAGTGG GGGTGGGGGG GACAACAGGG GCTGGGCTCT
3501 CTGGCAGACA TCCTCTGGCC AAGGATGGAA GGTGCAGGCA GGAACAATGG
3551 CTTGAGGCTG GATACCTCTC TTGCCCACAC AGCAGAGCCC TGGTGCATCA
3601 GAAACAGGGC TGGCATCTGG TGTCTCCAGT TGATGATGCA ATGCTTTGCT
3651 CTCTTCATCT CACCAGTGTC CTCTGACCCA TGGGTAAGAG AAGGAGAGAT
3701 GGCTGGGAGC CGAATTCTGG GATGTGAGGA TAGGTGATGT GGTGACTTCC
3751 TGCAGCTGCC TGACTGGGGC TTTCATTTCC TACTCCTTCC CTACCTGCGT
3801 AAATTTCCAT GACCTGTGTG ATAGCCTCCC TTTCCCTTCC TCACCTCCTT
3851 TTAACCTTGT CCCATCTTTC CCAATGGATA TCTTTCCCTG GCCAAACTGG
3901 ATGAGACTTG ATTTCTCGTT GATTTTTTTT TTTTTCCCCT CAAGAAGAGG
3951 ATTCTTGTGT AAAAGTATAT GCTTCAGACA GCAACTCCCC CTCTCCCAAG
4001 ATGGATATGC CAAGACTGGG CTCTGTTGTG TGGCCTCATG TGCCAGGTTG
4051 ACTTTGGGAC AGAGGCACAG ATGATAGGCA CAGATGCCAG CCAGAGGGGT
4101 CAGAATGTGT AAGTGCCAGC CAGTACTGTG TGGAGGTGGG AAAGTGGAAA
4151 GGGGCTGTCT TGGAGATGGA GGGAACAAGG TGGGGCTGGA CTATAGGTGT
4201 GGGCATGGGA GATGTGAACT CCTGGAGAGA TCTGGGCCAG GGTAGCCATG
4251 GGCTGGTTCC CATGGGGTTA GGGAGTGAGG GCCATGGCTT CCCTGCAGAC
4301 TCTCAGTTTA CACTATATAT TTTATAAAGG TGCAGCCACT GGAGCTGGGT
4351 TTCACTCATC GCTGTCTGCC TAGGTCTCCG CAGGTGTTGG ATTTCTGTGT
4401 CTGGGAATGT CGTGGGCCCA CCAGGGTCAT CTGTGAAGGT CTGAAGGGGC
4451 TTGCTGTGTT CACTGGGTCT TCCTGCCTCC TGTCTTTCTT GTTTGTGATT
4501 CTCTGGGCTA CAAACTGAAA AGATAAAAAG AGGGTATAGA GCTGTTTCTC
4551 CTTGGCATCC CTGGTGAGGT GGCTAGGAGT CAGGGAGAGG GATCACCTGT
4601 TCTTCTGGGG GGGTCCAATC GAGACAGGAA GCCTTCTTTT GGGCTGTTGT
4651 GTCTTGTCAC TGTGGCCTCA GAGGCCCACA TTGGCGGCTA GGTTGCAAGG
4701 TGGGGAGTTC ATGCGGATAT GCGTTGAGCA CTGTCTTTGT CTGCGGGCCT
4751 GTCTACATAA AGTCACTGAA AGTCACATAA CGTCACTCCG TTTGCTTCAG
4801 AACCGTGATA GGAGTGGAGC TGGGCTCTTA AGGGAGCCCA TGGTTCCAAG
4851 CTTAGCTCCA CTAGGCCGAA GGAGGCATTT AAAATAGGCT TGGATGCAGG
4901 AGCTAGTGGG CCAGGTGATG GCAATGATAA GTCGTTATTT TAAGATTTAA
4951 GAGCACCCCC CTCAAGGAGC CTGAGCCCTT ATGTCTTTTT TTATTTTTAA
5001 ATCTTCATAT TCCCTTCTTA TCTTTATTCA TATGCATACA GATTTTCACC
5051 TCGTGGAGCA TAACATTTTA TATCCTGCTC TCTTTGCTTA TATCCAAAGC
5101 ATTTCCCCCA TATTACTACA GTTGAAGGGC AAATGGTCCT TTCTTCTACG
5151 TCGTTTAGGA TTTATCCCTA AAACAATCAG CATCACAAGA AACTTCTGTA
5201 TATGTACCAT TTATCTGGAT TCCAGTTGCT TTTACCAAGA TAGATACTGG
5251 GGTAATGCCC TTGGCCTTAC TAAGAGATGC TACCGGAAAC AGTGTTTTGA
5301 AATCTGTTAT AATACTTTAA CATATTTATT TAATCTGTAC ATTCCGTGTG
5351 AAGAAATTTC TTTTGAAGCT AAATGTAAGC AAAAGCTTTC CTCTTTGTGA
5401 GGACCTGAGA GGTGAGGGAA GGGTCCTTAT GTGTTTCTAT ACTTCTGCAT
5451 GGGCAGGCCC TAGCGAAGTG CCTGACGTAT GCCAGCCACA TACACATTAA
5501 ATGAATGGGT CAAGAGGACT ATGTAACCAA TCATGGTTGC CTTTTGGCTT
5551 TGGCTCCTAG GAAACTCAGA GTCAAGTTGC CAGAGCCCTT GTACCCTGCT
5601 ACAGACTTGG GTCCTCCCTT TCTGATCCAG GGAGCCAAGC TGCAGACCTG
5651 ATACGGCTGC TGGAAGAGAG GACAGATGAG GATAAAGACC TGTGCTTGGG
5701 GCATAAGGCA GAGTGGGAGA TGTAGGCAGA CATTTAGCTG ATGATTCCTC
5751 CTTCCCTGTC ACTAAATGGC ACTATAGGGC CACTGTTGGG ATCTCTTCCA
5801 GGTAGTGATT TTCAATTTTA GTGTGCGTAA GGATCACCCT GAGTACTAGT
5851 TTAAAAAATA CAGACTTCTG GGCTTTAGCC ACAGAGATTC TGCTTTAGGA
5901 GGTCTAGGGT GGAGCTGCAG AATCTGCATT TTTAACACAT GCTCCAGTGA
5951 ATTTCATGCA GGTGAGGCAT GAGCCACTCT TTAAGAGATG CCACCTAAAA
6001 TCTGCAACAA CAGTTGCTCT TGCCATGCCC TCTGGAATTC AACAGACACA
6051 CCTTGGCCCA TCCTTCTCCA GATTGTGTGT CTGCCACTAT GTGGCCATCT
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FIGURE 3B

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6101 GTGCACATGG GCTGTTCTGT GATTAGGGGC CTCGTTCTGG GCCTCGGGAT
6151 TGGGGTGTCT GTGTCTGAGG CTGCGGCAAG CTGGGTGGCT CGGGTTGTGG
6201 CATGTTGGCC ACCAGAAGGG TAAAGGCTGT CCCTTTCTGG GTCCAGCTGG
6251 CCCTGGGGAC TGAAATGGGA TCCCCTGGAT GGTGCCAGCT GAGAGTCCCC
6301 GCCCCCTTAG TGTTGGCCTG AGTAGCCCCC ATGACATTTG TGTCCCCTGT
6351 GGTATCTCCA AGTGAGACTT TCCTGTTAAG GATCTGGGTG AAGTGAGGGA
6401 AAGAGAAGGG AGGGGGAAGC AGTAATGCAG GGAGTGGGAG AAGGAAGAGA
6451 AATCCACACA GCACTGGAAC ACAGGCCTCG AGGAAGCATT TAAGGAGGCT
6501 GTGTGCGAAA CCATGCTTTC CTCCTGAGGA TAAAACAGGC CAATTTCTGT
6551 AAACAGAGAA ATGGGCATCC TGCATATCAG TGATGGAGCG CCTCTACTTT
6601 CTCTCCTGAA GGGATGGAAG CCGACTGCAG GTCCCTCTGT GCAAAGGCTT
6651 CTGCCAGGCG GCTTTTGTCA CGCGGTCACG TTGAGCTGTG GGCCTTAGCA
6701 CACACAACAC TGGCCTGTCC CCCTCCCCTC CCACCTGTCT TCCTAGAGTG
6751 ACTTGGGGTG CTGCATCATG GTGTGGGGAT GGAGGTGGGA AGGTTGCCCT
6801 GTCCTGTCAG GGAGGCCCCT GCCTTCTTCC TGCTGCTTCC TCTGGTCCCT
6851 TGTCACCATA CCCTTGTTCG AAGCTGTGCT GAAACCCTAG AGGTGAGTGG
6901 CTGACCCCAT TCTCTGCTGA GACTGGAGAT AGGGAAGGGG AGGCTGGGTG
6951 TGACCATTCC TGCTCCCATC TGTATGCTTG CTGCTCTCTG AACAGCTTTG
7001 GCAGACCAAC AAGGGCCTGA TCCCATGGGT GCCAAAAGGG TGGTGACAGG
7051 AGGAGATGGG CACTTTGCAC CTCTTGAATG CCTCTCTGCA GAGCCCCTTT
7101 GTCACCTACC CATGGCCAGA CAGATCTGCC GCAGGACCGC TGGGGAAATC
7151 AAAGCACAAA AGCTTTGTCT GGGGTCTTTT TTTTCTTTTT TGGTTTTGTG
7201 CTGCAGGTGC CCATGACTTT GCCAGGGCTC AGACCCAGCG TCCTCAGGCC
7251 GTGTGGCCTC CACCCACTCC TTGGCGCCTT TCTTTAAAAC ACAGGTTCTG
7301 GATACTTTGT TCCTGTGATG AATCTTGGCA TATCACCTCA CACCTCTCCA
7351 TCTAGGCCCC AAGCTCCAAG CCTGGTGGAG CAAATCCCTC CTCGTTGCTG
7401 GCTGAGGCCC CATTCCCGTC TGTACCCACC TCTCTGGGCT GTGCGGTGGG
7451 GAGATTTCCA GCCACTCCTC CCCAACACCA TCTCCGCTTC CTGGGCCCTA
7501 TCAGCAGCAG CCGCAGCTTC CCATCTGCTC CCCTCTTTTC TCCTCCCTTT
7551 CTTTCCCTTC CCCCCTGCTT GCTGCTGCCC TGGGAGGAGC TATTTTTAGG
7601 GGCTGCTTCC TGGGATGTTT TACTTGGGGC TGGTTACCAT GAAGGAAATG
7651 TCACCAAAAC AGTGGGCAAA GGCTGCAGGC ACCGGGAGCC CTGCCGGGGG
7701 GCATGGAGAA CAGACGGCTG ACCCTTTTCT GGCCCTTGAG AGCAGCCAGA
7751 GTGCCCCCAG GCAGAGCCTT GCCTTCTTGG GGCTTGCTAG TGACCCCTTG
7801 GGGATTTTCT CTGTCAAAGC TGATTGAGGG CCTTTTCGCT ATAGGGCATT
7851 TCTTGGAGCC TCTCGCTTCC CTTGCCTTGA GATCCAGAGG CCAAAGTGGG
7901 GCTCAGGTCT TTGTGTCACC AAGTTAAAAC TGCTTGAGTG AGGGTTGAAG
7951 ATAAGGGGAG GATGCTGGGT ACATGCACAG AGCCTTGGGG GTTCACATGG
8001 GACCATTTCA GGCCCCGTCC CTCTGTATCA CAGCCCCCAG CTAGTCACCA
8051 GGTGTACATG TGTGAGGGCA TTAGAAACCA TGGTCCTGCT CTTGTGTGTC
8101 GGATGGACTT TGCTTTTAAT TGGAGACTCT TTGCATCTTT AGAGTGAGAT
8151 TCAAAGAGGA AGGGATGTGG CATCACAGTG TCAGGGTGAG GTCGGTGGGA
8201 TCGTGGCTTG GGATTCCCAC TGGTCAGTGT CCCAGGCCCA GGGCTGTGCA
8251 TAAGCAGCTG GGGAAGGTGG ATTATGACAT CAAATCCCTG CGATGTCCTT
8301 GTTTCTGCTC CTCAGAGTGC CAAGGGGACC AGACGGCGGC CTCTGCTGCT
8351 TGGGAAGAAG ATGAAAGGCA CTCAGGAGGG CAGCAAGTGA GGCCGCCTCC
8401 CATGGAGCCC TGAAATCAGT GGGGTTGCAG GAAGTTTCTC ACATCCATGT
8451 TTAGGGTCAT AGGCACAGAC CTGCAAAATA CCCTTTGCAA AGTTAAGAAT
8501 GTCTTTGAGA TTGGAACTTG GGAGAGTCCT CAGTCAGAGT AGGAATGTGC
8551 ATCCTTTCCC ACGTACAGAG GATTGTATGT TTACGTGGCA GCAGGATCTT .
8601 ATTTGAAGCT AGTGCTGGCA TTTGTGTTTT TTTTTTAGGA AAATGTCACT
8651 AAGTCAAGCA GGCCCATCCC TGAGAGGGCC ATGGAGAATC TGTGGCCAGC
8701 CCTCCCTGGC CCCCTGACCT GGCAGAGGAA GGAAAGGGCA TTGGAGTAGG
8751 CTTCTGTCTT CAGGCCAGAG GGGGAGGTGG TTCAGGGGCA GGCTTGGTGC
8801 ACCCCTTGGC TGCAAGCTAT CACCTCCCTA TCTGCTTCCT CTTTTCTGCC
8851 TCCCCTGGTG CATCTGGTCA CTTCTTGCTG CCCTTCCTGT GAAATCGTGG
8901 CACCTTGGAC CAAGTCCTGA AGCACTTGGG CAGAAGGCGG GAGAGGTTGG
8951 GTTTCTAGGA TCCTTGTTTC CCAGGGCCTG GCTCTGGCCT GGGCTCAGAC
9001 CACTCTGGTC TAGGCAGGCT GCTGGGGAAA GGCTGGAGCT GCTTCTGCTT
9051 TCTGCTCCTG TTGCCACCTC TGCTAATGAT GGGGAAAAACC TGCAGAGGGC
9101 TGTGGTTGGA GCTGGGCTGA AGGCCGGCAG GGGTGGGTCT CTCCATGGCA
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FIGURE 3C

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 9151 GTAGCACACA GGCAGGCAGG AAGTGGCCCT GTGCAAAAGC GGGAAGTGGC
 9201 AGTTGTCAAA CAGGAAGGGG GGGGCTGGGC TGTGGGAGGG GCGGGGATGA
 9251 GCCTGGGTAGA AAGGTGCGTG GAGGAGGGTC CACCTTGGAA GGTCTGAGCC
 9301 TCTCCCTAGT GGTTACTGGA AGGAGGGGTG TCTCAAGGGG AGACACCTTT
 9351 GCAGCACCTT GAGATGCCGA GCCAGGGCCC TCCCACTGTG GACCAAGCCC
 9401 ATTCAGTGGC CTCGCCCTTT TTGGGGTTGG AGATGCTGCG TCCAGCTGGG
 9451 ATGCCCTTGC TTTTGGGAAA GATGCTCTAG AAACCACTAC TCCATCCTGG
 9501 AACCCCTCTG CTGCCACTGC TGCTGGGATG GACCCTCTGC TTTTTTGCAG
 9551 CCGTGGGCCA GCCCTGGATG TGACTACAGG ACAGGAAGTG TCAGGGGAAG
 9601 AGACAGGAGA CAACAGCTGG AGAGGCTGGG TGGTGGCCGG GCAGTATGTG
 9651 GCAGCAGGAA CGGGGAGAGC GGGGCAGGTA GAAACTGCTC TGTTCATTGA
 9701 GGAGAGCTTG TGGATGGCAG GGTGCCACGG CTGCGAGGAA GAGGAGGGAA
 9751 GGGGACAGTG GCACTTCCTG CGGCGTTCCC CTCTCTCTGA GGAGCCCCTG
 9801 TTGCTGCCCA TCACCTGCAG ACTGTAGACA CAGGTGGGCC CCGCCAAAAC
 9851 AGGGAGGGAC ACTCCACCTC CAGGACTGCA ATGGAGGACC ATGTGGGGAG
 9901 CCCAGAAGCC AGGCAGGAGG GCTTAGTTGC TGTGTTGCAG ACCCTGCATC
 9951 TGCCTGGGCT GAGGGGACAG TGGGTCCCAT TCACAGTGTC TCTGGTGATA
10001 GCTGTGGCCA CAAGCCCAGC CCAGGAGACC CTGTCAAGCT TCTCACTGGG
10051 CCCTTGGAAA GGAGCTATAT GCCAGACCTT ATGCAAAACT CTTGACCTGT
10101 ACCACCTCAG TTAAACCTCA GATCTTGCTG TCTCTATTTT AGAAGTGAGG
10151 AACCTCTTGG CCGGGTGCCG TGGCTCACGC CTGTAATCCC AGCACTTTGG
10201 GAGGCCGAGG CAGGAGGATC ATAAGGTCAG GAGATCGAGA CCATCCTGGC
10251 TAACACAGTG AAACCCCGTC TCTACTGAAA AATACAAAAA AATTAGCCGG
10301 GCATGGTGAT GGGCGCCTGC AGTCCCAGCT ACTCGGGAGG CTGAGGCAGG
10351 AGAAGGGCGT GAACCTGGGA GGCGGAGCTT GCAGTGAGCC GAGATCATGC
10401 CACTGCACTC CAGCCTGGGC AACAGAGTAA GACTCCATCT CAAAAAAAAG
10451 CAAAAAAAAC AAACAAAAGA AGTGAGGAAC CTCTTTCCCA AGATAATGTG
10501 CCTGGCTCAC TGTCTCACCT ACTTTGGGTC CTAATCAAAT GTCACCTCCT
10551 TACTGAGGCT TTCTTGGACT GCCCTACTCA AATCTGCACT CCCCACTTTC
10601 TCTGCTTTTT CTACGCAGCA CTTGCCGTGA CATCTAACGT GCTGTTGAGT
10651 TTTCTTACTG TCCATCCCTC CCCCATACAC AACCCACTAG AGTGTCAGCT
10701 CCATGAGGGC AGGGATTTTT GTCTGTTTTG TTCGCCACTG TCTTCCTAGC
10751 ATCTTGAATA CTGTCTGTCA CATAGTAGGC CTCAGTAAAT ATTTCTTTTT
10801 TTTTTTTGAC TTGCTCTGTC ACCCCAAGCT GGAGTGTAGT GGCCCAATCT
10851 TGGCTCACTG CAGCCTCCAC CTCCTGGGTT CTAGTGAGCA CATTTGGCTA
10901 AATTTTGTAT TTTTAGTAGA GATGGGGTTT TGCCATGTTG GCCAGGCTGG
10951 TCTTGAACTC CTGACCTCAA GTGATCCACC CACCTTGGCC TCCCAAAGTA
11001 CTGGACTGGG ATTACAGGCG TGACCCACCG CGCCCAGCCA CGATAAATAT
11051 TTCTTGAAGG AATGAATGAA GCTCGGGTGG GTTTAATAGC TTGCTGGATG
11101 TGGCAGTGTT GGGCTCAATC CAGGGCTGTC TGACTTCAAA ACCGATGTGT
11151 TGTTAATTGC CATACTCCAC AGCTTAGAAT CAGAATGAGG ATCAAGGTAT
11201 AGTCCTGGGG TTCAGAGAAG ACCTGGGCCT TGCCCGGAAC ACAGGGCTCA
11251 GCTCCTTGGA GTTAAGGCTG AACTAAGAGG CTAACAAGGA CCCTCTGGAT
11301 GCTGGGCAGC TCCTTTGAGG AGCTGGGAGC CTGAGTCTGT GTATCTTCTC
11351 TCCACTCAAA GTCACTGGTA AAGCAGAGTG CCCTTATTTT TAGTGCTGTT
11401 GCTGTTGTGG GACTGTAACC ATTAGCTAGT AAGAGACTTA AGGAAGGAGA
11451 TAAACATTAA TCTTCTGGGC CTTCCCTCAG CTGCCACCTC CGCATTGCAA
11501 GATGCTGTTC TCCTGCACCT GCCCAGGCAA CCAAGCCTGA GAGTTATGGG
11551 CTGGAGGGTG GTGAGGTTTG TGCCCAGAGA GAGGGCCGTG GGTCTGTAGC
11601 TTTGGGGCTG GCTGGCTTGG TACCTCCATC TCAAGTCCAG GGATGGAAGG
11651 AAGGTGGGGT CATGTCAACA TCCTGCCAGA TCTGGAAGAA GCAAGCCCCC
11701 CAGCCACCAG GCAAGGCTGT TACAGCTCCC TTGAGTGCCT CGCTTCTGGA
11751 GGTCACTGGC CACATCCCTG TGCCTGGGAC CAAGGGATGC CAGGTGATCT
11801 GGGAGTTGGG AGTTACTTGG GGTTCTCCTG GCTGCATCCT GGTCGGTGGT
11851 CATGCTGAAC CCAGGCACAG GAAGGAAGGC CTGACCCAGA TCTTTGGGCA
11901 GCTGGGACGG ATTAGCTGGG CAGCAGGAAC TAATCTCTGT CTGTCCCCAC
11951 CTCTTTCCAC AAAGTAGAGC TGTTGCTAGA GGGAAAGTTT AGGACAAAGC
12001 TGGGTTTGGT TAGTGAAACA ATAAATGTGA ATTTCTTCTA GTCCATAATC
12051 CCTACATTAT CTCACACTGA CAGTCCTGAG TTTGAATCCC CCTTTTATCC
12101 CTTTCCTGCT GTGGGATCTT GGGCAAGTTA CTTAACTTCC CTGGGCCTCC
12151 GTTTCTTCCA TCATCTGGAA ATGTGGACAA TCATAGCATT TACCTAATGG
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FIGURE 3D

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12201 GATCATTGTG AGGGCTGTGG GAAGATTTAC AGAAGCTTTT TGCTGTTTAG
12251 GGTAGAGGCA GGGAGACAGG AATAGCTTGG CAGCTATGGA TGTGAAGGCC
12301 CCTGCCCGGG CCTGGATAAT TCAGGGTGAA CTGGACTCTC TTCCTTTTGC
12351 ACCCCCTCCA AAGCCTAGAG TCTTAACTCA ACTCTCACCA TTCTTTATCT
12401 GGCCATAATA GCACAGGGGT GGAGAAAGAG GGCTCTAGGC TCAGACCACC
12451 TGCATCACTG CCTGTTCGTG TTACCTTAGG CAGATTACTC TATCTTTTTA
12501 AACCTGTTTC CTCGGTAATA TAATAGAGCT AATCAGATCC CTACTTCACA
12551 GAGTTTCTGT AGGTATGAAA TATGGTAATC CATGCCTCTG CCTGACATGT
12601 AGTCAGTGCA TAGTAAGCGA TTGTTATGGC GACTACTGTT ATTAGTAAAC
12651 CCTTATTAAG CCCCTGTTTA CAGAAAGAAC TCTAGAAAGC ACTACCTGGA
12701 AAGGTACCCC CGCCTTCGAA GAGCTTGCAA CTGAAAGATA ACTGATGTAA
12751 TATATGATGT GAGAATCGTG AGAAGTGCAT TGGGAAATCG GGGGGGGGGG
12801 GGTGGAGTAG GAGGGAGAAG TCACAGTCTA CCGAGAGGAG CAGGGAAGAC
12851 TTCATGAAGG AGGTGACTTT TGGCAGGATT TCAGCAAGTA GAAAGAGGGA
12901 AGGACAGTGG GGGAGGGCTG TGAGGCCTCC GTGCTGTGAG TAGCATCCTC
12951 TCTTCCCACG TACTGGAGCT CTGCCTTCCT GTGGAAGGAA TTGACCCACG
13001 CAGCTCACTT GGATCTGGGG ACTTGTGGAT TTCTGGTTAT TCCACCAAAA
13051 CCAAGTAATC CTGGAGTCTG AATTTGAAGA GGTCAAAGCT TACAGCCATG
13101 GTGGCCAAGA GGACTCCGGG GAGAAGCAGG ATTTGTGTCC TGGTTTCTCT
13151 TTCTATAAAA TGGGCATCAT ACTAATGCCA CCTCCTAGAT TGTTATGAGG
13201 ATAAATTAAA AGAGGCAGCT GCCTGGTGTA GAAGTAAGCT CTCAATAAAT
13251 GTTAGCTATT ATTATTTTAA GTCATCATTA TCTTGATCAT CAACCTCTTT
13301 ATTATCAGCA TCATTATGTT TCAGGCTTGC CATCAGGACT ATGTAGAGAA
13351 TATATGCAAA ACCCCTAGCC AGTGCCGAGT ATATATTAGG TGCTCAGTAT
13401 AACTTAGCTA TTATTAGTGT TCCTAACAAG AAAGAGATTC TGGGCCAGGC
13451 GCGGTGGCTC ACGCCTATAA TCCCAGCATT TTGGGAGGCC GAGGCGGGTG
13501 GATCACCTGA GGTCAGGAGT TCGAGACCAA CCTGGCCAAC GTGGTGAAAC
13551 CCCGTCTCTA CTAAAAATAC AAAAATTAGC CAGGCGTGGT GGTGTGTGCC
13601 TGTAATCCCA GCTACTCGGG AGGCTGAGGC AGGAGAATTG CTTGAACCCA
13651 GGAGGCGAAG GTTGCAGTGA GCTGAGATCA CACCACTGCA CCCCAGCCTG
13701 GGCAACAGAA CGAGACTCCG TCTCAGAAAG AAAAAAAGAG ATTCTGGACA
13751 CCCTGGACCA CTGAAACCCT GTTGTGGTGG AAAGAGCACC AGAGTTTTAG
13801 TTGAATACCT GGATTCAAAT CCCAGCTCTG CTGCTCACTG GCTCGAAGTG
13851 TGCAAACCCT CAAGTCATTT CCTCATCTGG AAAAGGTGGT CATAACTATC
13901 TATCTGGCCC AGGCCTGGTG GCTGGTGCCT ATAGTTCCAG CTATTCAGGA
13951 GGCTGAGGTG GGAGGATTGC TTGAGCCCAG GAGTTTGAGG CTGCGATCAT
14001 GCCACTGCAC TCCTGCCTGA GGGACAAAGT GAGACCCTAA AATGAAAGGA
14051 AAACAAGTTG TCTCCAGGAT TGCCATGACT TGCTGCATTA CTTCAGCAGA
14101 TCATCACAAA TGCATAGTTA GTACCTGAAC TGAAGGAATA TGAATAACAA
14151 GGTGACCACA AGGAGAATGG ATGGTTGATG GCTTTTGTTT TTTCTCTTCT
14201 GCTTTTAGAT CACCAGAAAC TAGAACGTGA GGCTCGGATA TGTCGACTTC
14251 TGAAACATCC AAACATCGGT GAGTGCCTGG GCATGGAGCA TTTTGTGGGT
14301 ATTTTGTAGA AGCAGGGATA ACAGATATCC ACTGCTTTTG TGTGTGGGAT
14351 CACCTCTGTC TGTGGACCTT CACCTGGTGT CTGTTTTTAC ATGAGCAGGA
14401 TAGCAACTGT GTCTCAGAAT TCTGGGGCAT TCTAGTTTAG AGACCTGAGT
14451 ATCTGCATCA CTGCGGCACC TTCTCAGGGC TGGGGTGTGA GGCATCAGAA
14501 TAGGTTTCAG ATGCTATTTC TTCCCTTTCT CCTTCTGTCT TTGGGCTGAG
14551 GTCCAGGGTC CTCAGCGTGT GAGGTTCCGG GCTCCTAGCC TGCCAGCGTC
14601 CCTCACCAGG GGCCATCCAC AGCCCTCATG CAAGGGTCAG GATTTTGTTT
14651 GTGGACCTGA AAGAGTTTTG TTCCTGCTGC GGTGTCCTGC ACACTCTGGG
14701 GGTTTCCATG GTGCTCCCAT TTGTATTCCC CAGAGCCAGG AAAGCAAGCT
14751 GCCCCCCTGC CTGGCTCCTC TGGCAGAAGG GATGGCAGGA ACCACTCAGT
14801 ATGGGAAGG AGAAAAAAGA GGATTTCTCC CTGCTCCCAC CCTGACTGGG
14851 GGGACAAGAG CACATTGTTG GTTGTGCTAA AGCCTGAGGA GGTTTGCCTG
14901 CCTCAACCCA CTCTGGCTCA GTTTTACTTT GTTCAGCTGA AATGGTCTTT
14951 GCCAAAAGCG TTGGCCCTGA TTTGGTGCTC CTTGCAGAAG GGACAGAAAC
15001 TGGGCTGGCT GCAGTGTCTG AGCAGAAGCC CCAGTGTTGA CTTGAGGCAG
15051 AGCAAGGAGC ATCTCCTAGG TTTTCCCTGA AAGCCCTGAG TCATCACAAA
15101 AGACAACACG TGTTCTGTGC TCCTCAGGCA TGGCCTAAAT CTCAGGGCTC
15151 CCACCGTGCC CCAGAGGTCG CCTGCTCTGC TCTGTTGGCG GCCAGGGCTG
15201 TGAGGTGACT TGCTGAAGCC TAATGCTTCC TTCAGAGCTA CCCAGCCCCT
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FIGURE 3E

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15251 GGCTTCCCAG GTCTCGGGCT AGAACAGTCA AAGTGAGCTC TGTCATGGAA
15301 GGGCTGAGGT CCTGCTCTAG CCCTCTGGGA GAGGAGCAGC TCTGAGGTAG
15351 TCAGAACGTC AGCTGTGCAG GGCTTTCTAG ATGGCAATCA GCAGCTTGGA
15401 TTACACCCGA AGCAGATTGG TGTGGCCAGT GGTGATCGGC TTTGCCTGAT
15451 GCAGTGTGTT CTGCAGAGCC AGCACCTCTC AGCTGGTGGG TTCCTGGCCG
15501 CAGAACTACT GGAGCTCCTA GGTGGTTTCT GAGGTTAGGC CTTCACCTGA
15551 AAACAGCGCA GTGGGGACTG ACATGTTGCC TTTGGTAGGA GAGGGCCCAC
15601 AGAGGGAAAC ACCTAGAACA GCAGTCACAG ATTAGGCATG TTTTGCTTGG
15651 CTGACTCAGT GGTCTAAAAA TATTTTTATT ATTTGCCAAT ATTTAAAAAT
15701 GAGATTTCAC ATTTTGAAAA AAGAAAAAAT CTATTCCCCC GCCTTTCCAG
15751 TCAGAAGGCT TGGCTCTGCT GAGCCCCCAC CTTGCATGGC CAGAAGGAGC
15801 TGTGAGGAGC GGTGGCTGCC CCTGCAGCCC GCTGGCCACT GTCCTTGTCA
15851 CCCACTATGA GCTCACATTT GCATTACCCA CCTGGGCCCC TGTAGGCCTT
15901 GCAAGCTTGT GACCTCTAAC CTAGAAGTTC CAGAACAGGA AGAAAAAACA
15951 TGTGCGTGAC TAAAGCCACC CATAAGCACA GAAGCATTTT GATGTTCCAG
16001 ACCCGGGTCT CAATATCTGA GGAGGGTAAC TTCCTTTCCT TTATGCTCCT
16051 TGTGACCAAC TGGTACAGCA GTGATAATTT GTCCTCATGT AGGCAGGAGA
16101 ACAGCAGCTA GGGGTCAGTG ATGCAGGAAG CAGAACCATG TCCACATCAC
16151 CCGCGATGCG GGCGGGTTGA CCATGGGCGG GTTGACCACG GATGGGTTGG
16201 CCACGGACGG GTCAGGGTAT AATGAAGACA ATTGAGAAAT GAGCAGGAAG
16251 GACAAAAATA GAATTCTAGG TGAAAAAAGC CCTAGGTGTC TTTTTATTTA
16301 TTTCTAGAAT TAAATACATA CTTTTTTACC CCATAGACTT CACTCTGTTT
16351 GGTAGCCCTT TACTTTTACC ATCTGCCCTC GGCTCAGAAT GGAGGCAGGC
16401 GGAGGGACCA TATATCCTGG CCGTCTGCTC AGAGGCCAGG TGGGGCACAG
16451 TCACTCTTTT GGCCTCTGAT TTCCTAGAAC TGTGCTTCCA TTTCATGACT
16501 GCTCCCAGGT CCTAAGGAGG TTGGTCCGAG GACCGATTCT GGGGTTGAGG
16551 GTGGGCAGAG GGAAGGGGGA GTCAAGACTG TGTCCTGGGA GCTCCAGCAT
16601 CCGGTGGGAA CCAGGGCTGT TGGAGATGTG GCGGAGCTGC AGGTCCAGGC
16651 GGCTGTGGTT GCCATGGATC TGGACCTGGC TTGTGGCAGG AGAGGAGGCA
16701 ATTTTGTGCC CCTAATTCAC TATTCCTCTT CTCTCTCCAC TGCGCTGTCC
16751 TTCAGAACTG TGACCCTTTT GGCTCTGGCC TCTTGAACTC CATCCCAAAG
16801 GGAAACAAAC GGGCCAGCCC AAGAACAGTG CACAGTCGAG GAAGCTAGAG
16851 CAAAGAGCAT GTGGTCAGCC CTGCCTGTGG TCAGACTCGG AGGCACTGAA
16901 TTCAGATGGA GCATTTGGTG CTAGGGGCCA GTCATGCCCA GTTTCCCCTT
16951 AATAGCTAGT ATATTCTGTC CCAGGAGTTA AAAGCCTGTT GGAAGAGTGA
17001 ACCCTGATAT AAACTCTGGA CTTTGGGTAA TGATGATGAG TCAATGTGGG
17051 TTCATAGACG GTAACAAATC CACCACTCTA GTGGGAGATG TTGATGGTGG
17101 AGGAGACTGT GCATGTGGGG GACGTGGGGT ATTTGGGAAT GTTCTCGGGT
17151 ATTTGGGAAC ACCCTGTACT TTCCGCTCAA TTTTGGTGTG AACCTAAAAC
17201 TGCTCTGAAA ATAAAGTTTA TTAATTAAAA ACAAACAAAC AAACAACAAA
17251 ATGCCTGTTT GGGTGTAAGG CACACTGCCG AACTCCAAAC AGCGCTGGGA
17301 GTGTGGCCAG TGGTGGGGAG TTGAGAGGAG GAGACGCTGG TGTGAGGTCT
17351 GAGGTCTGAA TGAAGTCCGT TCTACCTGTG ATCTGCCTGC TCCCTGCTCT
17401 CAAGTCCTCT AATGAATAGA CTCTGTCTTC CTTCGTGCTG AGCTGCCCCA
17451 GCAGTTTCGA TCATAGTCTA GCATTGTGGT TTAGAGCAGC ACTTCTCAAA
17501 CTTTTATGTG CTTAAGACTC ACGCAGGGAT CATGTTAAAA TTCAGATTCT
17551 GATTCAGGGG GTCTGGGGTA GGACCTGAGT CTCCAGCTGA TGCTCATGCT
17601 ACTGGTCCGC ATGCCTGTCA ATACTTGGAG AAGCCAAGTT TTGCGGCTTC
17651 GGAGTCGCAT CCAGATTTGG GGTTTGAATC TGGGATTTGC TAATTAGTAA
17701 CTGTGACCTC TGGCAAGTTA TTTAACTCCT CTATGCCTGC CTCTGTTTTG
17751 TTATCTGGGT CCCTTCGTGG AGTTGTTATG AAAGGGTTCA GCCAGGAAAG
17801 GGGGCTAGGA GGGAGATGAT GAAAATGGAG ATTCCAGCCC CTAGAAGTGA
17851 TCTCTTCAAG ACCCCCAGCC TCGACTCAGT TCACAAGTTA TTCAAGCCTG
17901 ACCATTTACC CTTGAGCCCA GTACCCATTC AGCTAACAGT AAGTGTAGCA
17951 AAGAAACGGT TGCAAATAAA AAGAAACATT GAATCATGAC TGAGCAGTTC
18001 CTACATCCCT GCCCCCATGG TGGGGGTGGG GGGAGCCCTG CCACAGTAAG
18051 CTCTTGGGGG GCAGCTCAGT CCCCCACAAG CCCCCATGGC AACAGGACCT
18101 CCTTCCCACT GTGTTATTGC TGCAGATATT TTTAACAGCA CACTTTTTC
18151 AGTGCTTTTT GGAGAAAGAT TTGTTAGTTA AAATGTGGCA TATTGTTGGG
18201 TGGTTTTTAA AGAATTGGAA ATAGCCACAA CATTTGGGTT GTGGCTATCT
18251 CAGTCCTTGA AGACATGAAA TATCAAGTAA AGGTTTGTAG GTGTTTTGGC
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FIGURE 3F

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18301 CTGTTCTGTC TTCCACGGTT TTTAAAGAAC AGCAATTAGG TTTGTTGCTG
18351 AAATGCAGTA AATGCTTTAT ACTCCTTTCC CCAGATCTTC CTGTCTATGG
18401 ACATGGCCTG GCCCTTGTTG GCCTTCATGC CCTGTCTTTA CTCTGGAATG
18451 GGCTGGGTGT CAGATTATTT TATTCCACGC ATCCATAGTC CCTCTGCTCC
18501 TGCCTCACAG CATGACACAG TTGTGCTTAG TTAACGCATT TGTGTAATTG
18551 CTGGTTTAAA GCCTGTCTTC CCTCTTCGCC TGGCAGCTCC AGGTGGCAGG
18601 GCCGGCTCCT CTTCTTCACA GCCACATCCA TGGCATGTAC AGCCTCGCCT
18651 GCTCCGGGGT AGCTGCCCAG TGGACATTGT CGAGCCAGTC AGAATGGCCA
18701 CAGGTAGTGG GGACAGATTG GAGCTCCTTT GCCTAAGAAT TTGAGAAGGT
18751 GACTCCCAAG CAACTCTGCA ATATCAGGAA TCTTGATGTT GGTTTGTCTT
18801 GGCTTCAAGT CCCGGTTCTG CCACTTAGTG TGATTTTGGG CAGGTTTCTT
18851 ATGGAGCCTC AGTTTCCTCT CCTGTCAGAT GGGGTTATTT ATATGTAAGT
18901 AGCTACCCTG CAGAGCTGGT GTGAGGGTTC AATACAGTAA TGCACGTGGA
18951 GCCCATGGAA CGATGCCGGC ACACGGACAG CTCAACTAAG TGTTAGTTGT
19001 TAGATTTAGA TTGTTATTAT CAGAATCTGA TGGGGTGCGG TGGCTCACAG
19051 CTGTGGTCCC AGCCTCTCAG GAGGCTGAGA CAGGAGATGG CTCAAGACCA
19101 GGATCTCCAG CCCAGCCTGG GCAACATAGT GAGACCCTGT CTCTTAAAAA
19151 AAAAAAGAAA TAATGAATCT GCTGTTGCTA AATAGGCACT TAGAATGGCA
19201 CAGTCATTTC TCCTCTTGTC TTCAGTGTCC TGTTAATTTC TTTACAAATT
19251 AAAAAAATGT CGATAGCAGT CTTATTCAGA TACAGCTTCC TCCATCCCTC
19301 CTTGTCTTGG CAGGTGCCTT GCTCTGGGGC ACACATCAAA GCTGTTCTCT
19351 CTGCTGGGTG GCCTAGAAGG ATTAGTCTTC CTTTGCTGCT CCTTTCTTCT
19401 AATTCCCTTC CCCGGCTTCC TCCCACCTGG GCTCTGTGTG TGGCCTTCCT
19451 GGAGAAGGGC AGACGCCAAT GACTCCATGT CTAGGCAGAG GCCTGGGTGC
19501 CTGCACTTCT TGCCCTGTTC TTGGCCTTGC TGTGCTGGGC GGGGGCAGGG
19551 TGGTGTGGGG CATGGGGTGG TGTTGGGCAT GGGGTGGGGT TCTGGCTGAG
19601 GCAGGGCTCA GTGCCAGGCC CAGGCAGAGC TGAGTGGCTC CACTTCTCTG
19651 AGATGGTTGT CAGCATCATA CCTGCTGCTG TCCCGTTAAT TCCCCATGCT
19701 GCTGCTGTTA GTCACCTCCC TAATGGAGCT GGTCTGTAGC TTCTGGGACA
19751 GCTGATTTCC AGGGGATTAT TTGTATTACA CACTTTAATG CTTTTTAATA
19801 GCAAATTTTT AATTAAATGG AAAGTCCTTT TGGAAGCGAG GGAGCAGCAG
19851 CTGCAGCAAG ACTCAGCGTG AGGCACCGAC TTAGACCAGA GGTGCGCAAG
19901 TGAGTGGGGC GGAGGCAATG GCAGGACTTC GAGAGGACTT GATTGAGTGT
19951 ATATGGAGTG TGCCCAGGCT AATTTTTATG GGAGGAAGGC AGGGGCCTGG
20001 CGCTGGCTCC TTCCTCCTGT CCTAAAAGCC CCCTCTGTCA TCTGCAGGCC
20051 TAGGGAAGCA TCTTCTTTGC CCAGGAGAGA ATGTATATTG GATATATACA
20101 TTATATCCAA TAATGGGAGG GATATTGGAA GTATCACCTG CCTTTGATCC
20151 CGTTCCCAGA AATACTGAGA TTGGGATGGG ATTTTTGGGG TTGAGTCACT
20201 AGATTAGATC AAATAGTGTA GGTAATGGGA TGCGGAAACA GTCTTGAGGC
20251 CCTGGCTCCG GCCCTGGCAG GCTTCGGAGT CCTCAGTCAT CAAGGGAGGA
20301 GAACAAGGGG GCTATAGTGG TGGTTCAGTG CCTCGGGACT GTGCCGGCTG
20351 GGTTGTATAC TTTGCTTTCT GAATGATCTT GCTTCGTGGG GAGGGGACAT
20401 AGGGAAGCAC CTCAGCCCTG AGGAAACGTG TGACACTGGA AATGGAAGCA
20451 GCCAGGGCCC ACCCAGGAAG AGACATGGCC ATTTCTTTGT CTCCTAGCAC
20501 TGAACTGGTT AGTTTGGTGT CAGGCCATTC CTGAAGTGCT CCATGAGGTG
20551 CACCTGTAAC TGCCAAGGCT TGGAGCAAAG GTCAAACCGA GGGAGGCCTT
20601 TGGAACAGAA GTTCCCCATC AAGAGAGTTC ACGTGAGGGG AGGGACAGGA
20651 CAGTCAGCCA AAGCGGAGTC GTTTCTGCAT TAGAATGATG CTCAGGGGTT
20701 GGCATTTAAC CCAGAGGTGG CTTTGTGGGC AGAAACTTGA AGAGGAGACC
20751 TCAGAAGACT TCAGGTTGGT TTTTTACCCA AGAGCTTTGG AGGCGGGGAG
20801 CAGGGAGGGA TTCCGCCTGC CAGCTTTTTC TCGCAGCTGG TGCATCGCCC
20851 GAGTCTTCTT CCAGTGGCAC CCTCCCGGAC CTGTCTGCGA TGCTGCTTTA
20901 GGGACATTTG TAAGTGGTCT TTCTTTTGGA TGCCAGGGCT TTGTTGCCTG
20951 AATATGGGGG CTGCCCCACA TTTCTTAAGG GAAGCAGTGG TGTAGACCAC
21001 AGTCTTTGGA GTCAGGTAGC ACTGGATTCA CATCTTGACC CACCACTTAG
21051 AAGCTCTTTG GCCTTTGTTA AGAGACTTTG TGTCCCTGAG CCTCTGGTGC
21101 CCTCATCTGT AGAATGGGAA TAACATTCAT CTCAGGTGGT CGAAAGGAAT
21151 AATAAACTCC TCAAAGGCAG GCACTCTGTC TGTTCCTCCT GAATCCCGCT
21201 GCCTAGCGTG GGGTCCAGCA CATAGTAGGT GCTTGATAAA TGCTTGCAGA
21251 ATCAGTAATG TATGCAAGAG CCTAGCACAA GGCCTGGCAT AGTAAGCACT
21301 TAATAAGCTG TTATTGTTGT CATTGCCTGA ATGTGTGCGT GGCCTTCCAG
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FIGURE 3G

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21351 GCTCACCATC CATTATCCTG CACCACGTGC CTTCCTGCTG AGCTCTGCCT
21401 TTCCACCTTC TTCCCCACCC CTTAGTTCTG CTCCCATTTA CTGCTCTGGA
21451 AGAGCTCTCT GGCTTTCCCA TCTGGTCATT GTTGTCCCCT GCCGTCAACA
21501 TTGCTAGGTG CTGCTCACGC TGCATCTCAC CATCGTGCAT CATATCCCAG
21551 GACCACCTTC TCGGAGACCA GCCCTCTGGG AAGGTTCCGG CTTTTCTCCA
21601 TCTTGACTTC TTAGCCATGA AGCTTTTCTC TCTTGCCTGA GTCTGAGGTG
21651 GCAACCAGAG CGCCAGGCTC TGGCTCCCAG GCTGCATAGC CTTGCACTGG
21701 GGGGCACTGG GCACGTCGCC ACTTCCCCCC ACTGCTCCTT CTGGAGAGCC
21751 CTGTGAGCCC GACAGGATGG GGCAGGGGTG GGGCTGCTGA GGAGAAGCCT
21801 AGGATTTCCA AGTTTTCTCT CTGTTAATCT CTGTCCCCAT CTCCTCTCTT
21851 GCAGTGCGCC TCCATGACAG TATTTCTGAA GAAGGGTTTC ACTACCTCGT
21901 GTTTGACCTG TAAGTGCCAC TTTCTGAGGG TGTGGGGGCC TTTCCCTCTA
21951 GCTGACTCAA AATGAAGGCT CAGGAAGGGG CCTAAACAGG CTCTCCAGCC
22001 TCCGCCCAGG GCCCCCTCCT TTGTCCGAGG GAAAGGATTT GACTGGGGCA
22051 GATTGCTGCC CCCACCAAGG GGGTCTCCAT GTTCCCCCAG CGTCCCCCCA
22101 GGGCTCTGAA CCCCAGGACA GCATTCCTCT CGCCACTTCTG TTCAGCAGCA
22151 CGCCTTGCAC AGATGCCTTT GTCTTGTTTC TCAGTGTGCT GTCCTTAGTG
22201 AAGAAATAAA AGACAGCTCT TTGCATGACC TTAAAAATCC TGAGAAATCA
22251 GAGGTAGCTT TCATTAGTCG GAAACCAGGC TCCATTGGAT TGGGTCTCTC
22301 CTCCACGTTG GTTGTGGTTT AATGTCTTAA AAGTGGCTCT TACCTCCTGG
22351 ACACTCCTCT CCAGGATTCT CAGGGTTGGG TCTCTGTGTC ATTGGTCTCA
22401 TTACTCTTCA ACTTCAGTAG TAGCTCTGTC CTTCCTGGGC AGCGATATTT
22451 TAGTGTTTAT GTTGGTCTCA AAGCTGTGAC TTTTGGGGTA GGTTGACTGT
22501 TTTCTCTTAG ATCCCTGTAT CTTCATCTCT GCCTGACTAT TAGTGAATCT
22551 GTGCATTTTG GAAAAAGAAA TGTCCGGAAG GAAGGGACGG CCCATGATAC
22601 CTCAAGGAGA ATCCGGGTGT CACTGAAGGA TCGAGTGTGT TCTGAGCTCT
22651 CAGATGAAAT GCATGGGGAG TTGGGATTTC TCTGAAAGCC ATTCTACAGG
22701 GTGACCCTGT TTCTTCTTGG ACATTGGGGT TGGACAAAGG ACCCTTTCTG
22751 CCTCTGACCC TCTTCTTCCC GTTGGTTGCA GTGTTACCGG CGGGGAGCTG
22801 TTTGAAGACA TTGTGGCCAG AGAGTACTAC AGTGAAGCAG ATGCCAGGTA
22851 GGATGAGGGC CCGAGAGTTC AAATGTAGCT CTGGAGTTTA GGACTGAAGG
22901 AAGTCTTGGC CACCTTCGGG GTCCAGCATT GTACCTGTTT GAATAGTCTT
22951 TGGGGAAGAT CAGAATAGCT CTTGTCTGGA GAAAGATTCT GTTGAGCTGG
23001 GCTAGGGCTT GCATACTGTG GGTGATATTA GAAGTTAAAA ATTCAGCACT
23051 TCCTAACCAG GCGCAGTGGC TCATGCCTGT AATCCCAGCA CTTTGGGAGG
23101 CTGAGGCAGT TGGATCACCT GAGGTCAGAA GTTGGAGCCC AGCCTGGCCA
23151 ACATAGTGAA ACCCTGTCTC TACTAAAAAT ACAAAAAAAT TAGCCGGGTG
23201 TGGTGGTGTG TGCCTGTAAT CCCAGCTACT TAGGCGGCTG AGGCAGGAGA
23251 ATCACTTAAA CCTGTAAGCG AAGGTTGCAG TGAGCCAAGA TCATGCCACT
23301 GCACTCCAGC CTGCGTAACA GAGCGAGACT ATGTCCCCCT CCCCCCCCCC
23351 CACAAAAAAA ATCACTTCCA AATGAATGTT TTACAAAGCT TTTCCAAGTC
23401 TCCTTTACCC TGTGACCCCA GAAATACTTT TTTTTTGCAC TACCATGTAC
23451 TCGCCACCAT GCCCAATGTC CCCCTCTGCC CTTTTCTTTC CTTTGACAAA
23501 TTCTGGTGTG CTCAAGCCAC TGTGCTGAGG CTCTCGGCATG ATCCAGAGGT
23551 GCAGAAGACA TGGTTTCTGT CCTGAGGGAG TGGAGAGTTC TGGGCTGATA
23601 ATCCAACCAT AGAGCCCCGG GAGCTTTCAG CCTCTGTCAC CTTGTCCCTA
23651 GACCACCATG ACCAGCCTTG CCGTGGGGCT CCTCCAACTT GAGGACCGTT
23701 CCCCGGCCAC ATGCCTCAGC CTCTGCCCTC CCTGGAATCC CTGGTGCCTC
23751 CCTCACCCAC GCTCTCAGGT GCCTGTTCAG CCTGCCTTTC CCGCCTTGGC
23801 TCTTCCCCCA GCCTTGCTTT TCTCGAGGGT GATGTCCCTA CAACCTGGTT
23851 TTGATCATCC TGCCTGCAGC TTATCTGGCT TATGTGGCAG CTCTGGCTGC
23901 TTCTGGAGAG TGGGGGAGTG CAGCTTCCTC ACGAATTTCT CAACCTTGAG
23951 AGGCCAATGT TTGCTGATCA ACTTCAGATG CTTCAGCCTC GGGAAGAATT
24001 CTCAAGTGGG GAGATGAATT CCAGTGCCAG CAGGGGAGGA CGAGGCTCTG
24051 GGACGGAGGA GGCAGTGATG GCTCAGGGAG CCTGCGGGGA GGAGGGAGAG
24101 CTATAGGGAG GGGCCCTGA GGGGGGGTGA CTGTACCAGT GGGCTTGGCC
24151 TGGCTCTGCT GGGACACTTC GCACTTTTGC CATTTTTGGC CAGAAGGCGC
24201 TCCCTGCTAG CCCGGCTCTG TTCTAATTAT ACATCTCTGT GGAGACTCGC
24251 CTCTATAGCT CAGTCTTAAA GTTTCTGTGG CCCACTCTTG GGCTGTGTCC
24301 TATGGGGAGG CCCGAGTTTC AGCCCCCAGG GACCCAGTAC GACCCCTTGG
24351 TTCTTGTGGC ATCCCCAGCA TCAGATTTTA GGAATAGTAA GTCCAGGCCA
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FIGURE 3H

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24401 CCCAGCCCCA TACACTGGGA TGCTCTGCAG ATGTGCTTAA TATACCAGAT
24451 AGTGCCTGAT GACGGGGGTC TATATTCTAG GCCAAGTTCC TCAGCCTTGG
24501 TGCTACTAAC GTTTTAGGCC AGGTACTTCC TTGTTGTGAG GCCTCTCCTG
24551 TGCATTGTGG CAGACATTTA GAAGCATCCT TGGCCTCTGC CCACCAAATG
24601 CTGGGAGCAC CCCTCCTCCA GTTGTGACAA CCAGAAATTT CTCTAGGCAT
24651 TGCCAAATGT CCCCTGCGGT GGGGGGGGGC GGGCGGCAAA TTCATTCCCA
24701 GTTGAAAACC ACTGCTCTAG ACTGCCCCCG CTCCCTGTCA GGAGTTTGAT
24751 GACAGGGATG GCAGGATGGT TTGCTATGTG GACAGTCTGA TTTACGTGTG
24801 TGACTGTGGC TGGGCGCAGT GGCTCACGCC TGTAATCCCA ACACTGAGAG
24851 GCCAAGGTGG GTGGATCACT TGAGCTCAGG AGTTCAAGAC CAGCCTGGCC
24901 AACATGGTGA GACCTTGTCT CCACAAAAAA ATACAAAAAT TAGCTGGGCA
24951 CGGTGGCTCA TGCTTGTGGT CCCAGCTACT GGGGAGGCTG AAGTGGGAGG
25001 ATTGCTTGAG CCCAGGAGGT CAAGGCTGCG GTGAGCTGTG TTCACGACAT
25051 TGCACTCTAA CCCAGGCAAC AGAGTGAGAC CCTGTCTCAA AAATAAAATA
25101 ATAAAATAAC TTTGGGTTTT TTTCTCTACG CAAAATCATC AGAAGTGCTC
25151 CTTAAATGCC CTGTTTGGAA GCTCTTAAGT ACATTGTTTC TTAAAGGTAT
25201 CTTTGTACTT GTTTTAGCTG CCTTACTGGA TGCCAGACCT CAGGGCAGCT
25251 ATTGGGTCTT GTCCATCTTC ATTATCCTAG GCACTCAATA AACATTTAGG
25301 GAAATGAATG AGTGCACCCA CCGCCAAAGT AGCTTAGGTT GTTTAGTTGG
25351 ACTCTCCTTC CTAAGTTGCC AGCACAAGCT TCTTCTCCAA GAACAAAGTT
25401 ACTGTATGGA GAAAGAGAAA GAAGGAAGGG ATTGGATGCT CTCTTCTTCC
25451 TCAGGATTCT GGGCTGTCTC CTGATCTCTT GGAAATGAGT TGGTTGTGTT
25501 AGACCTTTCC AGTCAAAAGG GGGTGAGAGG AACCCGTTCT AGCGGTGATC
25551 CTAGAAAAAC CATTGCATCT GCCTGGGCCT CGGTTTCCTC TTTCTTTAAA
25601 TAGGTTGAAC AAGATGATGT GCAGAGTCTA AGGTTCCAGT GGCCGTTAAG
25651 TGATTCTCTG TGAATCCGTG GCCCCTTGTC ACATGCCTTA GTCTGCAGCA
25701 TGTGGTTGTG GATGTGGATG AGGTGGTTTA ACCCTGCGCT AACATTTCTT
25751 TTCCTTCTGC TTTTTTAGCC ACTGTATACA TCAGATTCTG GAGAGTGTTA
25801 ACCACATCCA CCAGCATGAC ATCGTCCACA GGGACCTGAA GGTACTACCC
25851 AGGCTCCCCT CCGTGCCTCT GCTCATGAAG TGTTGGCGCC ACCTGGTGCC
25901 AGATAGTGGT ACTGCGTAGG CCCAAACTAG GCTTCCTCTG GGCTGCAGGG
25951 TGGGTGCTCA CAAGGTTCTC TGTGTTTCTT CTGCAGCCTG AGAACCTGCT
26001 GCTGGCGAGT AAATGCAAGG GTGCCGCCGT CAAGCTGGCT GATTTTGGCC
26051 TAGCCATCGA AGTACAGGGA GAGCAGCAGG CTTGGTTTGG TAAGGGTGAT
26101 CCTGTCTTCC CGGAATGCAG CCCCCGCCCT TCCTCCTCTT CCTGATCTGC
26151 CTTCCTCTAT TAGAACTAGA AGCCAGACCC TTAATGGTCC TGGCCTCCGA
26201 GATCTCTCTT GGCCGTACGC GACTCAGTAC AGTAAGTCTA GCTGTTGTCA
26251 GCACTGCTTT CTTGCTGCCT GTGGGAAGGA GCTGGAGTTC CTGGTAGGCA
26301 TACGGCTTTG CCGTCTGGTT CAGATTCCAG GCGCTACAAG AAGCCCAGCC
26351 TGTCAGCTCT TGCTGCCCAT GTGCTGAGAG TTTATGTAGC AAAAGCAGCA
26401 GGAATAAGAT GGGACTTGGG GGAAATGGCT GGTGTGGATT TAACGAGAGA
26451 GAAAGTGGGT TCAGTATGCC TCTGCCCTCT CTTTTGCTAC AGGTTTTGCT
26501 GGCACCCCAG GTTACTTGTC CCCTGAGGTC TTGAGGAAAG ATCCCTATGG
26551 AAAACCTGTG GATATCTGGG CCTGCGGTAA GCCCATTCCA CGCTCTCAGC
26601 TTTTCGCTGT TAAGGGCCCT CAACTTCCGA TGATGGCAAG AAAGAGGCAT
26651 CGCTATTCCT TGCAGGTCAC ACACGTGCCT GGTGTATGTG AAATTATGGT
26701 GTTTGCCCCT GGGATGGCTG TTCCCATCAC ACCCTCCTCC CTGCGTACTT
26751 CTGGGATGAC ATTGTATCCT TCTTGGAGAG GGATTTGCCC ACGCCTTAGA
26801 GGATGGGTTG TGCCTAAAGA AATCCCTGGT GTGACTTGGT GACGTGAAGT
26851 GTGAGGCATA GCAGGAGGGG CTGGTAGCAT AGCATTATCG GCTGGCATCC
26901 ACTTCTGACT CTGGTATGGC CCCTGCCTTT CTAGGTGGCT CTGAGCCCTG
26951 CATGGTTTTT CTTGGTTCCT CAGGGAAGTA GGCGACTGAC CCCCATGACC
27001 TGTGTGTTCT GTCTCGTAGG GGTCATCCTG TATATCCTCC TGGTCGGCTA
27051 TCCTCCCTTC TGGGATGAGG ATCAGCACAA GCTGTATCAG CAGATCAAGG
27101 CTGGAGCCTA TGATGTAAGG ACCAGAGAGC CGGGCAGCCA GGCCAGGAAG
27151 GGCAGATGTC CTGCTCCTCG GGCTCTGTCC AAGGGAGCAG GCTTGTTTAG
27201 TGTGTCACGT GATACGGGGG TGTCAGGGGA CTTTGAGGAC CCAGGAATGG
27251 GCATCCAGGG CCCAATTCTT GCCACTCTAT GTCCCAGGGA GCAACTTTCT
27301 TTTGCACAGC CTTCTTCATA ACTAAAATTG AGGAGTCCAC TGAAGTCCTT
27351 TGATCTTTAC TTGCAAAGAA TGGAGCGGCC TCATTGGTGT GCTGTGTAAC
27401 ACAGGGACAA AAGGCCTGGA GACTCCCTCC ACTGCAGTGG CACCTTGGAC
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FIGURE 3I

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27451 ACATTGCTGA GCCTCTGTTC CCTCCTAAGT ATAGAGCTGG GCTTAAACCA
27501 GAGAATGTTG GAGTCCCCTT CCCGCTCTAA TCTGATGTTC TGGCATTCTA
27551 AAACATGACTG TTCTGTCTGT CTTTCCAAGT CTTTAAGTTG ACACAGGTTC
27601 TGGAATAGCC GCAGGGCTTC TCCAACTCTG CCAGTCACAG CTTTAGGTAC
27651 CACAGAGTAT CCCAATTACA GGAGTTGAGT TGAAGACAGA ACCAGTGTTG
27701 CAGGGTATGA AGCTCACCAA TACCACATTC TTCTCCCTAT TCCTGCTCCT
27751 TAGTTCCCAT CACCAGAATG GGACACGGTA ACTCCTGAAG CCAAGAACTT
27801 GATCAACCAG ATGCTGACCA TAAACCCAGC AAAGCGCATC ACGGCTGACC
27851 AGGCTCTCAA GCACCCGTGG GTCTGTGTAA GTGTCTTTGC TAGTGGCCAA
27901 GGAGCTCAGG GGTGTCAGCC TTCTGTGTGC CCTCGGCACC ACCCCCTCCT
27951 TCTTACCAGC AGAGATTCAT TCTGGGCCCC AAGCAATAAC TGAGCAGGCG
28001 GGCAGAGGAC TGTTGAGGGC CAGGGTCAAT AAATGTCACC AGGGAGACTC
28051 GGGAGGCTGA TGGGGCTGGT GGGCCACTGC TCCTCTCTCC CCCACTCATG
28101 GCTGTCAGGC TGGGATTGGT TCTGTTCTTG GATGAGGGCT CAGGTTGACC
28151 CTTGTGGACT CCAGGTAGCC GGTGATAGAA AGCAGCTGGC AAAACCCAAA
28201 GTGAATTCCC AAGCTGGGGT TCATACTCAG ATCTCAACTC CACTGGAGTG
28251 GTGACCAAGA TCCAACAAAT CAACAGAAGG GGTTTCTGAG TCATTAAAAG
28301 CATAAAAGCT GAGGCATAAA GCTTCTGCGC TAAAGTCCTA GGAGAGTCCT
28351 CTAGGCTATC AGTGTGGGTT GACGTACTCT GTTTTTATAC ACAATTCTTT
28401 CAAGCTGAAA TATCAACTTT CAGACAAAGA AGAGGATTTG GTAGAGTTAG
28451 GCATCTTGAC AACCACGAGG CATTATTTAT CTGTCCATTC TGTGTTTATT
28501 AAATACCTCT TTGGTGCTGG TTACCGTCTG GGTGCTGGAG ATACAAAGAT
28551 GAATGAGGCA TGGTCCCTGC CCCAAAAGAT CATCTAGGGA GACAGGCACT
28601 CAAACAGGCA GTCATGTTAC AATGTGACAA GTAGGTACAA GAATCTAATG
28651 AGAGTACAGG AGCTCCTACT GTTCCTGGTG GGTGGTGGGG TTACTGAAGG
28701 CTGCACGGAG GAGGTGACAC CCCTGTGCTT GTTCTTGGCA AATAACGAGG
28751 TCCTCAGAAC GTTAACCTGC AGACAGAGTT TAGCACAGTG AGAGGTTATG
28801 GGAAACTATG GTGAGTTGAA GGAATGTTGA GTTGTTTGGT TGTCGATGAG
28851 GCTGCAAATA TCAGAATGCA AGAGAATGGG GCAAAAGATT CCCTGACATA
28901 CAAGTTTCTG CCTCAGGAGT TTGGATTTTA TTCTGAAAAC ATAGGGAATC
28951 ATTTAAGGGT TTTAAAGAAG AATGAAATTT GCATTTAAGA ACACTTTGGA
29001 AGTTGTGAGG AAATGAATTG CCAGGCATGG TGGCATGTGC CTGTAGTCTC
29051 AGCTGCTGGG GATGCTGAGG CAGGAGGATC ATAAGCCCAG GAGTTTGAGG
29101 CTGCAGCGAG CTATGATTGC ACCTGTGAAT AGTCATTGTA CTCCAGCCTG
29151 GGAAAGATGG TCAGACCCCA CCTCTTTAAA AAAAAAAAAA AAAAAAGAAG
29201 GGAATTGAAA ATTTTTAAAA GAAAAGGGCT GGAGACAGAG AGCTCAGGAA
29251 GCTTTTTTAA TAGTTGGAAT AGTCTAAGCA AGACCAGGTG AGGTCTCAGC
29301 AGAGGGTAAG GATGGGGGAA TGTGCAGTGT GTTGAAATTC AAGAGATATT
29351 TGAGAGAACC TAAAGGATTT AATTCTCTCC AGTTGGATTT GGGGGGAGCA
29401 AAGAAGAGAG AGGCCAGGTT TCAAGTTGAG CGGAGAGTTG TACCCTCACT
29451 GACCCAGAAG AAAACCAGAG GAGGAGCTTG TTTGTGAGAC AAGACGATGG
29501 TTTTCTCTTT TTTTTTTTTT TTTTGAGATG GAGTCTCGCT CTGTCGCCCA
29551 GGCTGGAGTG CAGTGGCGCG GTCTCACTGC AAGCTCTGCC TCCCGGGTTC
29601 ATGCCATTCT CCTGCCTCAG CCTCCCGAGT AGCTGGGACT ACAGGTGCCC
29651 GCCACCACGC CCGGCTAATT TTTTGTATTT TTAGTAGAGA TGGGGTTTCA
29701 CCGTGTTAGT CAGGATGGTT TCGATCTCCT GATCTCATGA TCCACCCGCC
29751 TCGGCTTCCC AAAGTGCTGA GATTACAGGC ATGAGCCACT GCGCCCGGCC
29801 AAGATGATGG TTTTCATTTT GTGCCTGCTG AGTCTGGCAA CCTCCAGCCA
29851 GACACATTCA GTGGGTGGTT AGAAATATGG TCCTAGAGAT TAGAAAAGAA
29901 GCTAAAAATT GGAAATCCAC ATTGTAGTCA TTTCTGTGTA GTTGGTAGTG
29951 AGGCTGTAGA AATAGCCTCT TCCTATGCTG TAGATGGGCC TGTTCCTATG
30001 CTGGTTGAGT TCTTACGGTG AGCTTCTATT GGCTGTAGTA GAGAAGAGAC
30051 GGCCACTACA CACCAGCATT TAATGATAGG GAGAGTTAGG GGGCCCAGCA
30101 AAGAGCACTG AGAGTGAGAC CTTCCAGAAG ACCCAGAAGC TAAGAAACAG
30151 GGGGTCTCAG TAAGGGAGCG TCAGGAATCA GATGCAGAAG AGTCCCTGAT
30201 TAAGTTGGGG AAGAATCCCC TGGCTCTGAC CATTAGATGC CATTGTTTCA
30251 TCATTTCACT GAGACAGTGG AGAGAAAGAT GAAACCCTGT TTTCAGTGAG
30301 ACGAAAAGGG AGTGAGGGTG AGGAGGGGCA TGGGGAGCTA GGCATTGAGG
30351 TGGGAAATAA ATGGTGATAC TTAGATTAAG ATGGGCCAGG GGAGCTTTTA
30401 ATGTAAGGCT CACACCTGTA ATCCCAGCAC TTTGGGAGAC CAAGGCAGGC
30451 GATCACTTGA GGCCACGAGT TCAAGACCAG CCTGGCCAAC ATAGTGAAAC
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FIGURE 3J

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30501 TCCATCTCTA CTAAAAATAC AAAAAATTAG CTGGGTATGT TGGTACACAC
30551 CTATAATCCC AGCTACTTGG GAGGCTGAGG CATGAGAATC ACTAGAACCC
30601 AGGAGGTGGA GGTTGCAGTG AGCCAAGATA ATGACACTGC ATTCCAGCCT
30651 GGGTGACAGA GGGAGACTCT GCCTCTAAAG AAGAAAAAAT TTCTTTTTAA
30701 AGATTATATT GGTCAGGAGC GGTGGCTCAC ACCTGTAGTC CCAGCACTTT
30751 GGGAGACCAG GGTAGGTAGA TCACTTGAGC CCGGAAGTTT GAGACCAGCC
30801 TGGGCAACAT GGCAAAACCC CATCTCTACA AAAAAAAAAA CTTTAAAAAT
30851 TAGCTGGTTG TGGTAACGTG CCTTAGCTAC TTGGGAGGCT GAGATGAGAG
30901 GATCACCTGA GCCTAGAGAG GTGGAGGTTG CAGTAAGCCA TTATTGTGCT
30951 ACTGCACTCC AGCCTGGGCA ACAGAGTGAG ATGCTGTTTC AAAAAAAAAA
31001 AAAAATTTTT TTGTTTAAGG AGAGGCTTAA CTATAATCTA TAGAGAAGAA
31051 TCTAGTCCAG AGGAAAGAGT TGAAGATCCT TGCTAATTGA GGAAGCAAAG
31101 GTTTGGACAG CAGAAAAAGA GAGGGGGCTC CTGAGCCAAG GGCAGGGGGT
31151 CCATCCCGGG GATGACCATG ATCCCCCTGA GACTTCTATT AGTGTGGAGG
31201 CAGGTGAAGA TCGGCTTGTG AGTGGAAGTC TGAGCTGAAA GGGGTTCTTG
31251 CTGATGACCT CTCATTTTGC TTTTGGAGAA ATTTACACCG AGGAGGAGGT
31301 AAAATGAGAG ACTTGGGGAA GGTAGAGAAG GTGGGGAGAG TTGCCTCCGG
31351 ACCTGGAAAG AGTGGGCCAA GGGTGAGGGA AAGGATGCGA GGAGGCCCCG
31401 TAGTGTTGGT GGGCACCTGG CTGCAGGTGC CAGGATTTGT TTTTCTGACA
31451 GGCTGGTGAA GACAGCAACA GCAAGGGGAG AGGGCAAGCA ACCTGAAACA
31501 GGCACCCAAG AATGGGGGAA ATATTCTGTT CTGGGGTCAT TTTTGCAGGC
31551 CCTACCCTCT GCAGTCCCGT GTGTCTCGAG CCCCTGAGGA CATCACTATA
31601 TTCTGAAATT ACATAATGAT GCTGGTATTG ACAGCTGAGT CATTGAGGAA
31651 GTGTAGACTG TGTCCCATGG ACTCTGTTTA AGGAGGCCAG GAAGTTAGCA
31701 GTAAATACAT TGAAGACAAA TTTCCATCCA AAAAAGGCGG GGCACAGTGG
31751 CTCACACCTG TTATCCCAGG ACTCTGGGAG GCCGAAGTGA GCAGATCACT
31801 TGAGGTCAGG AGTTCGAGAC CACCAGCCTG GCCAACATGG CCAACCCTGT
31851 CTCTACTAAA AATACAAAAA TTAGCTGGGT GTGGTGGGAT GTGCCTGTAG
31901 TCCCAGCTAC TCGGGAGGCC AAGACAGGAG AACCTGAGAG GCGGAGGCTA
31951 CGGTGAGCCG AGATTGCACC ACTGCACTCC AGCCTGACTG ACAAAGCGAG
32001 ACTCCATTGC AAAAAAAAAA AAAATTACA TCCAGAATGA TGAAAAGAAT
32051 TGATGCTTCA AGGTGACGAT CCTTAGCTTC TGGGATCATG GCTTCATTCA
32101 GGACCTTGCT GGGGGTGTGT GGAGAGGGGC TCTTGGAAGG AAGGAATGTC
32151 CTCTGTAGAG AGCAGGAACC CTGCCGTTCT CTCGCTGCTG AGCATCTGGA
32201 ACGCAGTAGG TGCTCAGTAA ACAGCTGCCT AAGGAGTGAC TGAATGAGGA
32251 TCACAGCCCC CAGGGTACTC TCCTGTTCGG TAGCCTCTGT TTCCCAAGGA
32301 AGAATAGGAC GGTCTCTCAG CAGCCCGTCT AGCATCCGTT ATGGTGTTCT
32351 CACGTTCATG TTGTCCTTAT GTAACCTTGA GTTCGGGTA GTGCTTTTAT
32401 TCTAAAAGCG TTTTCACATC TGTGACCTCA TTTCATCTTC AGAGCAACTC
32451 TGGGGTGGCT GAGTGCATGA CCCTGTCCTG GGCATGGTAT CGGTGCCAGG
32501 ACTGTGGGAG GCGCAGAGGA TCTGGGCTGG GGCTCATAGC CTGTCTGTTT
32551 GGTTTCTAGC AACGATCCAC GGTGGCATCC ATGATGCATC GTCAGGAGAC
32601 TGTGGAGTGT TTGCGCAAGT TCAATGCCCG GAGAAAACTG AAGGTGAGTG
32651 TCGTTTCTAG GCTGCCAGCC TCCTTGACAT CATGCCTTGC ACCAGTGTGG
32701 CTCCTGCCCC ATTTCAGAAG GAAGCTCCCC TCCTGGCTGG AGCTGGGCTC
32751 TGAAGGTTGT ACATGTCACA GGGGAGGGGG CCCAGAGGCC TGATGTCTTC
32801 AGGCTCTAGC CAGGACCTGC CTTTGCCTGA GACCAGCCTG CCCTTTTCTA
32851 GGGTCTCAGT GAATTCACAG GACCTTCCTC TTTCCCCAGG GTGCCATCCT
32901 CACGACCATG CTTGTCTCCA GGAACTTCTC AGGTATGTTT TCCCAGCTGT
32951 GTACTTTGAT TATGCCGAGG TGAGTGGATC AGGAATGGGC TGTTGCCATC
33001 CCGGGCACCG CTGGGTTTCC TCGGCGTCCT GGGCCACACC TTGACCAGGG
33051 CGAGTGAGGA TCCTGTTTTG AGGGGCTGCT GCTGCTGCTG AGTCCTGCTC
33101 CTGAGATTCA GGGGGCTGGA CTCACATTTG TGAATTGTTT CCTAGAACTT
33151 CCCAAGGAGT AGCCTGCCCA ACTTGCTATG TACCTTGTTT CTCCTGGATTC
33201 TTATTTAACT CTCTGAAGAC TCTCAGCACT TTACAGATTT TAGCCATTCT
33251 AGGATCTTGG AGGATGTGCT GGGGGAAGAA AAGAGAGATG AGGTACAGTG
33301 AGTCTTCTCA ATTGCCAAAT TGCCACCATT CATTTGCCTG CTGGGACGAT
33351 CTCTTACTTC ATTTTGTCCA AGTGGAGATG ACTAATAGAA ATTATTCCAG
33401 ATGTTTAAAC CTTTTGTGGC GACTTGTGCT TAAAAATAGTC CCTGAGATAC
33451 TAGCTATAAC AGTGAAGAAA TAAAGACCAG CAGGAGAGAG GGAAAGGAAC
33501 TTGCTTAAAT TTGCATAAAG AATTGGGAGA GGTGGGACCA ATAATTTGTA
```

FIGURE 3K

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33551 AATCATACTT GACATTTATT TTTAAGATGC AAGACACTCC ACTCCCCTCT
33601 TGCCCCCACC CTCACCCCAA CCCCTATTAT TGTTTGCCTT CAATTGGGAA
33651 GCACAGTGGC TTTTTTGTGA GGAAAAGATT AATGTCGAGA CTGAAGACAG
33701 AGAGGGCTCT GCCCAGCTTG CCATCTCCCC CGGTCCTCCC TCCCTCTAAC
33751 CCCTTGCCTC ACTGTTTTGG TTCAAGACCC CCCCTTCTCC TTCCCATAAT
33801 AAGACTCCCT CCCTTGCTTC CCCTCTGCAC CACCATGGAA AGGGGGTTGT
33851 GTGGGAGCCT AAGCCACCAC TCAGTGGGAG CCACTTCTGA ATACCCGTCC
33901 TGCTGGGCTC GCCTGCGCTG GCTCCAGGTA ACGCCAGGCC CTTGGCTGTG
33951 AGGATGCTGC AGGCAGGGAG CCTAGGGCTT CGTGGTGTAG CCTGAGAGCC
34001 ATGGAGCTCC GGAAGGCCAC GGCTGGATAG TGAGCCCGGG GCTGGTGGTG
34051 CCCTGCCCTA GGCCTTCTCC TTTGACCCTG GTTTGGGGCT TGATCTTGTG
34101 TCATGGGTAC CCACGACGGG CATACTGTGG TGTGGCTCCA CCTCTCGCAG
34151 ATGGGAACAG GGAAGCGTGG CTGGCTGCCT CCGGTGGAGT TGCAACTGTA
34201 GTCCCACACT TGCTTCTTGT GCTTTAATGA CGCAGCTTCT ACTTTTTGGG
34251 TCTACGAGCC TTTCCAGAGG ACATTGAAGG GCGTTTCGGT GTTGCCCCTA
34301 GAGCGAAGCT CTGTCCTCTC TCCCCTCTGA GTTGAAGAAA TGTGAAGACA
34351 GTCTGCTGCT TCTCTTTTAG CCCAGCCAGT CAATAGCAAG GGCCCTGTCT
34401 TGCAGCCCCG GGCTCCACA TCAGCCTCCC CCTCCATTTC AGGAAACTGG
34451 CATCCTGGTT TCAGGAAATC GGGTGTTAGG ACAAAGCATT TTATTCATCC
34501 CTGTAGAGCC TCCTGTTCTT ATTGGCCAGA CCTAGACTGG CCTTTGAGCT
34551 CACTTTGCCT TGGGTCAGAG GAGACAAACA ATGTTGCAAG CATTCCAGGA
34601 TGGCCTCTTC TGCCCTGACT CTGGGACAGG TGAGGACAGA GTCTGTCCGG
34651 AAGCTTCTGC AGAAAGAGGT GTCTATGGAT GCAATCAAGA AGGAAGGGCA
34701 CCTGTGTGTT TCTCTAGGGC TGTTTTTTGA GTTGACCTCC AATAGGAGAT
34751 GTGGCTTATC CTGGACTCTA GCAGTTTGGC TAACAGCGAA TCGGGGCCTC
34801 CAGAGTGTAT TGCTTCAGCA GCCTTTGTTT TCTTTCTCAG GGTTTATTTC
34851 TTGGGCACCT TTCACCTCAG CACACTGTGA CACACAGACT GAGAATGCTG
34901 CCTCTCTCGG CTACCTCCCT TAAGACAGGG ACCTGTGTCT CTGAGGGGTT
34951 GGGGGGCATG GAGCTGGGGC CCACCAGTAA ACTTAGCTGC ACAAGGGCCA
35001 CAGACCCTCC CTGGGACCCC CACGCCAGTC CCTCTAGTGT GTGGGATGTA
35051 GAGAGGGGAG AGGGCTGCTC TGCGCCCCCG GCACTCTCAT CGTGGGCTCA
35101 TTTAGCTTCT AGGGAGGGAA GGACTAGAAG GGAGGGCGTT TCATCACAGC
35151 CTTAAGCTAG GGCCGGGCTA CCTCAGAAGG GGCACCTGCC TCTCACCGGC
35201 TCAGGCATTT CGCTGTGGAC CCTCCTCCGG AGGGGGTCAT GAGACAGGCA
35251 CTGCAGCCCT CTCCATCTGG TGGGGACGCA GTGTTCCCTA TGCCCTGGCC
35301 CAGCCCGGTC TTCCCAGGCC CCCAGACTGC TGCAGGGCTG GCTCGCGCCTA
35351 CCTCCTCAGC CTGCCCCTGG CGCTCCGCTC CCCCAGCTCG GCTGGCTTGG
35401 CCACGCCGCC TGGGCTGCGC CTCGCGCTGG GGCATGCTCG CTGCTGACGG
35451 CCCCGTGGCT TTGCGGGGCT CTGTGCACTG AGAGACTGTA TCCCCTCAGT
35501 TGGCAGGCAG AGCTCCGCCC CGGCCTCGCC TGCCGCGAGC GCCGCCGGCC
35551 TGGCCGGGCA AGGTACGTGG CATGAGTCCT CCCCGACGGC CTGCCTCGGC
35601 CCCCTGCCAC CCCACCAGGA GGGCCAGCAT GCCGGGCCCA CTCACCAGGG
35651 AGGCGAGTCC CATGCTTGCG GGCTGAGATG GGCATGCCAG ACAGACTACC
35701 TAACTTGGCA TCTGCAAGCG CATCGTTGTT ATGGAGCCCC CTAACCAGCC
35751 ATGCATGCTG GGCGCTTGCC AACTTTCAGG GGGCAGTAGC CTGGGGGCAT
35801 GGAGCTGGGC AGCGGGAGCC TTGCCAAGAG CCCGATGCCC TGGGAGGGCT
35851 GCAGCCAACA GTGGGCCCTC AGAGACAGTG CTGGGCATTG CCCTGAGCTG
35901 CCCGGTGCTA GGACTAGATT TCCGCAGCAC TGTTTAAGAC CCCACAGAGG
35951 AGCCGCGCTC CTCAAAATTG TGAAGTCTGG CGCTTGCTGG CCTCCAGGTC
36001 TGAAAGGCTC CAGAGTGCAG AAGCCTCAGA GCCAGCTGTT TCTGGGTTCA
36051 CATCCTAGCC CTGCCACACC CTGAGCGAGT CACACCAGCT CTCCCAGCCT
36101 TAATTCCTCA CCTCTCCAAT GGGGATGATA AATAACATGG TGGTGCTTAA
36151 GATCACCCTG TCGAAGGCTC TCAGCCCTGC CTGTGCAGTA CAGCTGTTAC
36201 CTGGGAGCTC GTAAGAAGTC CTAATGCCAG GACCCCACCC CAGACAATAA
36251 AATCAGACCC TTAGGGATAA GATAGGTAGT ACGCTTTTTT TAAGCTCCCA
36301 GGTGATCCTA GTGGGCAACC AGCGTTGAGA GCTGGCTGGT GAATGGAAAG
36351 CACTTAGACA GTAGGCGGTC AGGCACAGGA GTCAGCACAT TTAAAAAACA
36401 ACATTCAAAC CCAGCACGAC AAGATAAGAT CAAAGGTCTT TTTCTGGAGT
36451 CAGAATTCTC GTAATGGAAG GACCCCTGTT CTCACTGGAG AGAGATGGAA
36501 CACAGCTTGG GGAGGAATGG CTACCCAAAG GGCAGGAGGG TGGCAGCAAT
36551 AGTGACAACG ATGGTGGACA CTTACTCAGT ACTTGCTATA TGCCAGGCAC
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FIGURE 3L

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36601 TCTAAGTGCT TTTCATGCAT AATCCCACTG GATTCCCACC ACTGTTTTGT
36651 GATGTCAGCC CTACTTTATC CCATTTTATA GATAAAGAAA TTGAGGCTCA
36701 GAGAGGTTAA GTAACTCACC AAAGGTCACA CAGCTGGCAA GTGGTGGAAC
36751 CAAGATACAG ACCCAGGGCA GGCAGTCCAG GTGTATCAGA CAGTTGGGCT
36801 GATTCCATCT CCCTGTGCCT CCCAGACTCT CCTCCCCACT GTCTGCTACC
36851 TTCCTGTGGC CTTTTGTGGC CAGCTGGTGT CACCAGCCTT CTGGCACAGA
36901 GCTCATCAGC CTGGAGCGTC ACCCTATGCC TGGCTAGAAT CTGTTTGACA
36951 GCTCATTATT CTGCCGAGTC CTTCCTGCTC ACAGGTCCAG AGAGTGGACA
37001 CTGGGGAAAG GGTGGCAGCT AGGACCCAGT GAACCTGGTG AGGACCTGCT
37051 CAGTGAAGGC TTCAACCCCC TGGCAAAACC CTCCTGTAGG TGGTCCTGGT
37101 TTCTGTGTCT GTGTCTGTCT GTCCTCTGGT CTCCTGTGTG AACTGTGACA
37151 CTCTGCTTCT TGAGAACACT CAGGAGATGT CTTGCATCCT TGCAGTTTGG
37201 CCATCCAGAG AACTTCCATG GCACCTAGGG ATGGAGCCCT CACTCTTTCA
37251 CCCTGGCACT CTGCTTCCAG GCCTGGGTGG AAGCTGTCAA AGGCAGAGTC
37301 CCCAGTGCCC CAGGCGGCTC CAGTACTGAG CATGGTTTCT CCTCTAAGTG
37351 TCGTGCATCC ATGCCCTCCT CCACGCAGAG GAGATCCTGA GGTGCCACCC
37401 TGAGGGCTCT GACGCCACTC AAGATCCCCT TCTTGCTGAG AGGCTATAGG
37451 AAGTGCCTCT TTTGGGGGTT TCGGGAGACC CTTGGCCCCC TTGTCAGACA
37501 CAGCACTCTC TTGTGGATCT GGCTGCCGGA CTTCAGGTTG GGGAGAGGGT
37551 ACAATGCAGG AGACTTGATA TTCCTCTTTG TTTTCACAGC TGCCAAAAGC
37601 CTATTGAACA AGAAGTCGGA TGGCGGTGTC AAGGTAAGTG TCTCCAGCCT
37651 CTGAACAGAC TGGCCTCTTT CTCCCCGCAG TCACTATGGG AATTCTTGGC
37701 ACCTGGTTCC CCCTTTCCCA GGGAATCTTC CTATCCTTGC TAGTCTGCTT
37751 TAAACCAGAT GCCTTTGTGC TCAGAACAGA AGGTTCTGCT GGCCTGAGAG
37801 GGAAGTAGGG AGGTATTTTT CCTGGCCCTA GCTGGATGGG AATGACTCAG
37851 GGGAAGTGAT CCAAATCATA GTTTATACCA GAGCTGAATC CGGAACCTGA
37901 CTTCTACACG GATGCTTCAT CTCCAGGGCT TGACTCTGGG TTTTTTAGGT
37951 CATTTGGTTA TCTTTCTTTT TTTCCTTTTT AGAGCACAAA TCCTTTTAAT
38001 CAAATGAAAG CCAAATTTGC CTGAGTGATT CAGGCAGGGT ATAGGGCTTG
38051 GAACCTGAAA CCACTCTCCT TTTGGTCTTT TTCCTTCTCT CTACAACACT
38101 TTCAGATCCC ACTGAGTGCA ACAGCCTCGA GCTTTCTTGA CGCATAGGCT
38151 CCTCAGAAAA AGGCAAAGGC CATGGTGGAT CACGGCTTGT TCCCACTGGG
38201 TGAGGGAGCT TTTCCCATGG GACTGGGGCA AGAGGAGGGA CCTGGGACCC
38251 ACCAGGAGCC CTGCTGGGAA TGGCTGCTTG GCCAAGGTAG AGGAGAGGTG
38301 ACTGGGGCTA CCCACAGGGC CCAAGACATT CTGTAGATGC TTTGGGGGCA
38351 GAAAGGATCC TGGGGCTAGG GCATTGGGTA GGAGCTCATG CTATCTTGAA
38401 GCCTCCCAGC TTACACTCTA GACTAGATTT TCACTGGGCC TTTTCCCAAG
38451 ATCTTGTGTC AACAGCTGAG ATACACACAC AAGCCCCGTT CCCTCCCCGT
38501 TCCCTCCCCA CTCCCTCCTC TTTCCCTCAT TCTCTGCATG CCTGCTTCTG
38551 TGTTCTTCCG CCCCTCGCAG GGGAGCCTGG GCTCCGCGCA CACCCTCTGA
38601 CATGGAGCTG GGGGCATCGT GCGGTCCCCA AGCTCTGCCC CTGAGCTACA
38651 TGGATGGAGC CAGGTGAGGA AAAGGGGCAG GTTTAGTTGG AGAGAGTGTT
38701 TAATAAGTAC CTGTCAGTCA GATGTCCACG CAGCATTCTG TTCTGACGGG
38751 TACACAACAG AGGTGTAAGA GGGGGTGTGG CTTTCAGTCG CCATAGGAAG
38801 GGGGCCGCAC CTGGAGTCAG CTGAGCGCTG CTAGTGGACC CACGCGAGAT
38851 GGTTTAGTCC AGGAAGCTCA TAGGAGAGAG CGTACTGGAG AAAGCTGCAG
38901 GGACATAGGT GAGACTCACT TTGCAGTTTT ACTTTCTGCT ATATGTTTTC
38951 TTTAAATTGA AAATATGGGT CAGGCTTGGT GGCTCACTCC TGTAATCCCA
39001 GCACTTTGGG AGGCTAAGGC GGGTGGATCA CCTGGGGTCA GGAATTCAAG
39051 ACCAGCCTGG CCAACCTGGT GAAACTCCGT CTCTACAAAA ATACAAAAAT
39101 TAGCCAGTCA TAATGACCGG TGCCTGTAAT CCCAGCCACT CGGGAGTCTG
39151 AGGCAGGAGA ATGGCTTGAA CCTGGGAGGC GGAGGTTGCA GTGAGCCAAG
39201 ATTGCGCCAT TGCACTCCAG CCTGGGCGAC AGAGCAAGAC TCCGTCTGAA
39251 AATAAAGAAA AGAGAAAAGA AAACAACATG ACATTTCTAT AACTTAAAAA
39301 CAACAAATTA TATTTGTATG GGTTCTCTTA TACATATTGA TGTTCTCTGC
39351 CCAGTGAGAA CACAGGGTGT GTGGTAGATT GATGTCAAAA ATATGGTTGG
39401 ATCAGTCTTA TCAGGCAGAA TTGGAAGTTT CTGTGTCAGA CCATGGGAAA
39451 TACCATAGGC CATTGAGCAG GGAAGCTATG GTGAGAGTGC TGATAGAAAT
39501 GATTTGGCAA GCCGGGTGCG GTGGCTTCAC TCCTGTAATC CCAGCATTTT
39551 GGGATGCTGA GGCAAGAAGA TTGCTTGAGT CCAGGAGTTT GAGACCAGCC
39601 TGGGCAAAAC CTTGTCTGTG AAAAAAAAAA AAAAAAATTA ACTGGGCATA
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FIGURE 3M

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39651 GTGGTGTGCA TCTGTAGTCA CAGCTACTTG GGAGGCTGAG GTAAGAGAAT
39701 TGCCTAAGCC CAGGGAGTTT GAGCCTGAGG TGAGCCAAGA TCAAGCCACT
39751 GCACTCTCCA GCCTGGGTGA CAGTGAAACC CTGCCTCAAA AAAAAAAAAA
39801 AGATACCTGC TGTGCCCCTA GAAGTTGGGA AGGCAAAACT TAATCTACCT
39851 TTTAAGGTGT TTACAGTGGG AGAGACACAA GGCAGCTACT GTTTCTATGG
39901 AGTCTGCTAA GGTCTCAGGG AGGTGTGCAC CTGGCAGGTG CTGGGGGAGC
39951 AGACAGATAA ACATCCAAAC CAGGACAGGA ATCTTCTGGA AGGAGATGGC
40001 CAGGAATTGA GCTTGAGGGA GTAGCTGGAT TTTGCTGGGT TAAGGAGGAG
40051 ACAGGAGGGG AGGGATATTC CAGGCAGAGG GAAGAGCGCA TGTGAAGATA
40101 CACGAGGTTG AAACAGCATG ATGATTCTGG GAACTTCAGT ATCTTCTTTA
40151 TGGCTGAAGG GAAGAGCAAT TGCATAAAAT GAGACCTGAA ATAAAGCAGT
40201 GACTGTTGAG GTGGAGGGGA GAGGATGGAA AAGGCACCAT TACAGAACAG
40251 GTTTCTAGCC AAACTTTCTA GATACTACTG GTGTCAAAGA TGAAGGTCAT
40301 GTGCAGCCAT GTAAGATTAG CCCAAGGAGC CAGCTCAAAC CATGCACATC
40351 CAGGGCCCAG CTTGGAATTC ATGTTCTGGA GGCCTTGGCT GGGAGGCAGA
40401 ATCTGTGAAT TTTAAAAACA CTTTCATGAA TCCAAAGCAC ATGAAGGTTT
40451 AAGAGTCTGG TAAAGGCAAA ATTTTGGGGT TATGTGTTAA GAAAGGGCTG
40501 GAACAAGAGT CGGCAAAGGA AACAGAGGAA GGACAGAGAG GTAGGGGGAA
40551 AAGAGAAATG TGCAGCAGCT GCAGCTCTTC CAGGAACCCT GAGGATGAGG
40601 GCTGGGCAGA CACATCATTA GGTAAAGGCT TTAAATGAGG ACGTGCGTGG
40651 GGAACCTAGC CCTGCAATGT GTTGTGTGTC TGACCCTGAT ATGTGCTCAG
40701 TAAATGAGTT TTATGCCACA TTCTTTTGAG AAAAGAGCTT CAATATCATG
40751 GTGGGAACCA GAGGCCAATG ATCACCCAAA ATTAAAAGGC CAACCGCGTA
40801 TTCGCAGCCG TTGTGATGGG AGGGGTTAAT ATTTTTATTG AAAGAGTTTC
40851 TGTGACAAAT AATCCCTCTT AAAACCCAGT AGAAGCTGGG CGTGGTGGCT
40901 CACGCCTGTA ATCCCAGCAC TTTGGGAGGC CGAGGCGGGT GGATCACGAG
40951 GTCAGGAGAT CGAGACCATC CTGGCTAACA CGGTGAAACC CCATCTCTAC
41001 TGAAAATACA AAAAATTAGC CGGGTGTGGT GGCAGGCGCC TGTAGTCCCA
41051 GCTACTTGGG AGGTTGAGGC AGGAGAATGG CGTGAACCCG GGAGGCGGAG
41101 CTTGCAGTGA GCTGAGATTG TGCCACTGCA CTCCATCCTG GGTGACAGAG
41151 CAAGACTCCG TCTCAAAAAA AAAAAAAAA AAAAAAAAA ACCCAGTAGA
41201 TAGGCTAGGT GTGGTGGCTC ACATCTGTAA TCCCAGCACT TTGGGATGCT
41251 GAGGTGGGCT GATCACTTGA GGCCAGGAGT TCGAGACCAG CCTGGCCAAC
41301 ATGGTGAAAC CCCCTCTCTA CTAAAAATAC AAAAAGTAGC CAGTAGTGGT
41351 GGTGCACGCC TGTAGTCCCA GCTACTCGGG AGGCTGAGAT AGGAGAATCA
41401 CTTGAACCTT GCGGGGGGCA GAGGTTGCCG TGAGCTGGGA TTACACCACT
41451 GCACTCCAGC CTGGGGGACA GAGCAAGACT CTGTCTCAAA AAAAAAAAA
41501 AGGAAGATAG ATGATCAAAG AAAATAAACT GACAACCTGA AAACAAGGAA
41551 GTAGAACTGG ATAACAAATG TGGAAAAATT TCTAGCCTCA CTAGTATCAG
41601 AGAAATGCAA ATTGAAACAA GGTGCCATTT TTGGACTCTA GTTAGTGATG
41651 GTAGTGAAAA CCAGAATGGT CCTTTCTAAA ACAGCCTGTG TGTCAAAACC
41701 ATAAAAATGC TTCTACCTCT TTTTACCCTG TTAATTCTAC TTCTGAGAGT
41751 TTTTCCTAAA GAAATAATTC AAAATAGGAA AAAGCTAAAA GCAGAAAAAT
41801 GTTGAACATG ACATTATTTA TAGCTGTGGA AAGATTGGAG GCTGGGCACA
41851 GTGGCTTATG CTTGTAATCT CAGCACTTTG TGAGGCCAAG TTGGGAGGAT
41901 TGCTTGAACC CAAGAGCTTG AGACCAGCCT GGGAAACGTA GTGAGACCCC
41951 ATCTCTTAAA AAAAAAAAA AAAATTAGCT GAGTGTGGTG GAACGTGCCT
42001 GTAGTCCCAG CTACTTGGGA GGCTGAGGTG GGAGGATTGC TTGAGCCCAG
42051 GAGGCTGAGG TTACAGCCAG GATCACACCA CTGCGCTCCA GCCTGGGTGA
42101 CAGAGTGAGG CTCTGTTTAA AAAAAAAAA AAAAGAGAGA GAAGAAAAA
42151 AAGATTGGAG ACAATTGAA AAGCCAGTAA GGAGCCAGAC ACAGTGGTGC
42201 GTACCTATAG TCCCAGCTAC TCAGGAGGCT GTGCAGGAC AGAATTGCTT
42251 GAGCCCAGGA ATTCGAGGCC AGCTGGGCAA CATAGTGAGA CCCCCAACTC
42301 TTAAAAATGT TTTTAAATTT AAAAATAAAA AGATTTTTTA AAGCCAGTA
42351 AATGACTAAA TAATTATGGG AAATCTACTT AATAAACTAT TCAAAGTTA
42401 TTAATTTTCA TGACCGTAGG GATATTTTAA GTGAAAAATA AAGTGCAGAA
42451 ATGTTTTATA TTAAGTGAAG GAAGTGGTAT ATAAAGGAGT ACAGACAAGC
42501 CAGGCACGGT GGCTCACGCC TGTAATCCCA GCACTTTGGG AGCCCGAGGC
42551 AGACAGATCA CGAGGTCAGG AGATCGAGAC CAGCCTGGCC AACATGGTGA
42601 AACCCCGTCT TTACTAAAAA TACAAAAATT AGCTGGGCGT GGTGGTGCGT
42651 GCCTGTAATC CCAGCCACTT GGAAGGCTGA GGCAGGAGAA TCGTTTGAAC
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FIGURE 3N

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42701  TAGGGAGTCG  GAGGTTGCGG  TGAGCCAAGT  GCGCCACTGC  ACTCCAGCCT
42751  GGTGACAGAG  CAAGATTCTG  TCTCAAAAAA  TAAAAAAAAA  AAGGAGTACA
42801  TACACTATCA  TTCTAAATTT  GGTTTGAAGA  AACGTGTTTG  TAGATATTTA
42851  TTCAGTATAT  AATATGTGGA  TAAAAAAGGG  ACTGGAAGAA  AGCCCACTAA
42901  GTGTCAACAG  TAACTTCACC  AGGTGATGGG  AATTTGAGAA  ACTTTTTTGC
42951  TTACACATTT  TTCTGTATTC  CTATATTTTT  CATCTAGATT  GTGCACTACT
43001  GTTATCAGAA  TTTTTTTTAA  ATACTATTTT  TTTTTTAAAG  TAAAGCATAA
43051  TACCAGGTGT  GGCAACTCAT  GCCTGGTAAT  CCCAGCTACT  GGGAGGCTGA
43101  GGTGGGAGGA  TTGCTTGAGC  CCAGGAGGTT  CAGCCTGGGC  AACATAAGCA
43151  AGACTCCATC  TCAATTAAAA  AAAAAGAAA   AGAGGTAAGA  CATGTGCTTG
43201  TATTATTATA  TCTTATAATG  ATATCTTTTT  TTTTGTTTTT  TGAGACAGGG
43251  TCTCACTCTG  TCCCCCTGGC  TGGAGTGTAG  TGGTGTGATC  TTGGCTCACT
43301  GCAACCTCCG  CCTCCCGGGC  TCAAGTGATT  CTTCCACCTC  AGCCTCCTGA
43351  GTAGCTGGGA  ATACGGGCAT  GTGCCACCAC  GCCCGGCTGA  TTTTTGTATT
43401  TTTAGTAGAG  ACGGGGTTGC  CCAGGCTAGT  CTTGAACTCC  TGAGCTCAGG
43451  TGATCTGCCC  GCCTCAACCT  CCTGAAGTGC  GGGGGTTACA  GGCATGAGCC
43501  ACCACGCCTG  GCCTATAATG  ATATCTTAAA  AGATTGCTTT  CTTTTTTTTT
43551  TTTTTTTTTT  TTTTTTAGAC  GGAGTCTCAC  TCTCACCCAG  GCTGGAGTGC
43601  AATGGCATGG  TCTTGGCTCA  CTGCAACCTC  CGCCTCCCGG  GTTCAAACAA
43651  TTCTCCAACC  TCAGCCTCCC  AAGTAGCTGG  GACTACAGGC  GCGTGCCACC
43701  ACACCCAGCT  AATTTTTATA  TTTTTAGTAG  AGACGGGGTT  TTGCTATGTT
43751  GGCCAGGCTG  GTCTCGATCT  CCTGACCTTG  TGATCCACCC  GCCTCAGCCT
43801  CCCAAAGTGC  TGGGATTACA  GGCATGAACC  ACCGTGCCCG  GCCAATTGCA
43851  TTTTTTAAAA  AGACTGGAAG  ATTGCTAGGA  GTATTAGTGG  TTTTCCCATG
43901  CCCCTTCTCT  GTTTTCCAAA  TTGCTTGTAT  TGTGGCTGCA  GTCCTTTTAT
43951  AATATGAAAC  AGGTAAATAA  CAACTTATGT  TGTGGCTGCA  TCAAAGGGGT
44001  GAGAAACGAA  AAGGAGAGGA  CAAAGCAAGA  TGTGCAGAGT  TCGACCTTTC
44051  CAGGCTCTCT  CAAAGTCAAG  GTTTTGATCA  ATGTTATGAG  GGAGGCCTGT
44101  GAAGTAGCTC  AGATGGTCTT  GAGCTTTCAG  CATCATGGAT  TCTTCTTTTA
44151  GATCCCATCT  TCCCTTCCCA  ACTCCCCCTT  CCTCAATTCC  TACTGCTTAA
44201  GTGTCCATAG  GGCGATTTCT  TTTTCACTGT  TCAGAAGCTT  TCTGCAAGAT
44251  GTTCAAAATA  CTAGCATTGG  TTTGAGCAGC  TAGTCTGTCT  TGTGTTCTTG
44301  ATTTGGGGGA  CTTAGCTTCT  ATTTAGATTT  CTTTGAAGCT  GGATGCCAGT
44351  GACCCAGGGT  CTATGGAAGA  GTAAGAGCCA  CTTGTGAGGA  TGACTGAAGA
44401  GGCCACAAAC  TCTCAGATCC  TGAGAGTGTA  GGACAACTTG  TGCCTTCTGC
44451  TAGTCCCAGG  CCAGAATGGC  CATCCTATCT  TTAAAAAAGA  AAGCAAGCAA
44501  GAAAAACGAA  AGGTTATAGT  TATTTCCCTA  AGTACTATTT  GAATTATTTT
44551  GTTAAATTAA  GTATGAGAAA  GAGGTTTGAA  CGCTTTTCCA  GCTTAAAATT
44601  TAAAATAAAT  ATACAGTTTT  TAAGTAAAAG  TGAGATATGA  TTCTTTAGAA
44651  ATCATCTGGC  ATTTAGCCAG  GCATGGTGGT  GTGCACCTGT  AGTCCTAGCT
44701  ACTCAGGTGG  CTGAGGCAGG  AAGATCCCTT  GAGCCCAGGA  GGTTGAGGCT
44751  GCAGTGAGCC  ATGATCATGC  CAGTACTTCA  GCCCGGGCAA  TAGAGCAAGA
44801  CCTTATCTCT  AAAAAAAATAA  TAAAAAGACC  TCACATTTAG  ACAATGTGGT
44851  AGTGTGCTGG  TTCAGAAGGA  GCCCAGCTAT  GCATGGCTAA  GGGCAAATCC
44901  CTGAATGGAG  AAGGAAATTG  AAAAATGTTG  ACTAACCTGA  GAAACAGTCT
44951  TTGGAAAAGG  GTGATCTCAG  GTTCTCATGC  AGGACAATTT  AGGAAAAAGA
45001  GAGCAAGCCA  GGAGAAGGCT  GAGAACTTAT  TCCCCATTAG  TCAAAAATCT
45051  GCTTTAAGTC  AAGATCCTGC  AATGGCCTTT  CACAACAAGC  CCCTGAAAAT
45101  CAGCAGAACA  AAGACTGGGC  CTGGTGAGTG  AGTGCCTACG  CAGAGTTCTT
45151  GCTGCCGTGA  TTCAGTGCAA  GTTAGAAACC  TGTGCTCTTC  TTTAGCCTGG
45201  GGAAAAACCA  AAGTCAGCAA  ACCCAGCTCA  ACTCAGCAAA  CTTTCGTCGC
45251  CTGTATGCTA  ACTATAAGGC  ATGTTGCTAG  GTACTGTGGA  AATTGTAAAG
45301  ACACATAAGA  TAGGAACCTT  CCTGAAAGCA  GTAACACTTT  AGTTGGGTAA
45351  AGGGATAAGG  AGATATACAC  ACACACACAC  ACACACACAC  ACACACACAC
45401  CCCACTACTT  ATATATATGA  ATATAAGGGA  ACTCCTTCTT  TTTGAGGGAT
45451  GATTTTCGAA  GTAAAATATC  ATATTTGAGC  ATATTTAAAA  GGCCACTGTA
45501  AGGCTGTGTG  CGGTGGCTCA  CGCTTGTAAT  CCCAGCACTT  TGGGAGGCCG
45551  AGGTAGGTGG  ATCACCTGAG  GTCAGGAATT  CGAGACCAGC  CTGGCCAACA
45601  TGGCGAAACC  AGTCTCTCTA  CTAAAAATAC  AAAAAAAAAT  CAGTGGGGCG
45651  TGGTGGCGGG  CGCCTGTAAT  CCCAGCCACT  CAGGAGGCTA  AGGCAGGAGA
45701  ATTGCTTGAA  CCAGGGAGGC  GGAGGTTGCA  GTGAGCCGAG  ATGGTGCCAC
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FIGURE 3O

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45751 TGCACTCCAG CCTGGGCAAC AGAGTGAGAC TCCCTAAAAA TAAATAAAATA
45801 AATAAATAAA TAAATAAATA AATAAATAAA TAAAAGGCCA ATGTAAAAGA
45851 GGCCTAACTA TATTTAGGTT TTTCTTTTCC TTTAAATCTA ATTCTAAATT
45901 ATGGACCATT GTCAATATTT GTAGCCTCTT TCGTTGATTA TAATAATAAT
45951 CCCTGAAAAT GCCTTCTAAA GAATGCTGGC CGCTTGAGGG CAGGAGCAGT
46001 TTATCAGCTG TGTTTACCTG AAACAGCCCT CAGTGTTTGC TGGGCATTGT
46051 TAAATGAATG TGCAAAAGTT GAACGACAGA CGGACATATT ACAGGGGGAC
46101 CTTACCCCCA GTGAGCTAAT GATGACATTG ATAATTACCC TTCATTTTTT
46151 AGACACAGTC TTCTGGGATA TATTTTCAGT GTTCCACGTG GTCTTCATCT
46201 TGATGCGTCT GTTTCACATG TGAACGTAAA GTTCGTGAGC ATCTAGTTGA
46251 GGCTGAGGAA TCACTGCTTT CAACATTCCC TGTGGCTTAC ATCCCTGCAT
46301 TTTTATGATC ACTGTAGTTT TAATCACTGG CACTCCTGTA TTTCTATTTT
46351 CCACGAATTG CAAAATGCAA TAAAAAATTC AAATATTGTA AACAAGCATG
46401 GCTATACTGA CAAAGGAAGG CCAACATTTA ACTGCTAGGT GATTTTCAAA
46451 AGCTCAGCAT CTTTATGTAA AAAGCATAGT AGGGATGCAG CGAAGTCAGA
46501 AGTCAAATTT TATTAGAGCT GAGGAGAGCC TGTAGTAGCT TTTGCTTTTT
46551 CCCTGGTGGC TGCTCACTTG AATTTCAGAC AGTTCTAGTA ATGAGAGAAA
46601 ATAAATAACA TTACAGGGTG AGCTAACCCT ATGAACCCAG ACCTGTAAAT
46651 TTGTAGCAAA ATGATACTTA ACCTCACAGA CTTGTGTCTT AATCTCCTTA
46701 AGAGGCTTTT TTTGAGCAAG GCTGAGACAT CTCAGAAGAT ACTAAATCTG
46751 TGTCTATGAA CCTGACCACA AAAGAGTTCT TCCCTCCCAG GGTCTGGAGG
46801 GTGTGAGTGC CTGTCGGTCC GTGTGCTGTT TAACCCTCTG GTGCTGGACT
46851 CCGGGTCTCC CTCCGCTCTT TTCTCCCTGA TGCAGAGCCC ACACTGGTGC
46901 GCTAACCTGC AGCGTCTCTG TGCTTCTCTT CTTACCTCCT CTTTCCCCTT
46951 CTCTTTCCCT CTTGCTGTGG TGTGTCCAGA AAAGGAAGTC GAGTTCCAGC
47001 GTGCACCTAA TGGTGAGCCT TGCCTGCCCA CCCATCGCCC ACTCCATGCT
47051 GCCTGTGCCC GCCTGCCAGC CACGCAAACC TGTTCTGCCA CGTGCGTGTG
47101 CCTCACTCAT CCTCACTGCA TGTCTGTGCT GTGTGGGCAG GTGTGGCCTG
47151 TCCTGCCAGG CGGGGGCCAT TGCCCAAGGT CACCCAGTAG CCTAAAAAGT
47201 GGACATTGGA AGGGGTGGTA CGGCACCCCC TGCTGTGGAG CTTGGACAGA
47251 CCCCAGCGAC CCAGGGTAGG ATGTGAAGCT GGTAGGGACT TGGGGCAAGC
47301 AAGGGAGAGA CCCTCACTCT CTTGTCACCC AGAAGGAGAG GCCCTGCTTC
47351 CCAGGCATGA GGAGCTGCTT CCTACAGACT GGCAGCTGGA GGGCAACTGT
47401 GTGGTGGGCA GAGGAGCTGG TTGCAGGCTC CCACTTGTGA GTCTCGCTCT
47451 CCTGGCTCTG CCCCCGTGCA AATCCCATTC TCTCTAGCTG TGCCCAGTGG
47501 TTTATTCTGC CCACCCAGCC CTCGGGGGAC AGCTAACTCA TCTTTCTCAC
47551 GGGACACTGG GCACCAAGGG CAACACAGCA GCCTGAGTCA TTATGAAACC
47601 ATCCATTAAA ACCAGAGGTG GGGGCCGGGC GCGATGGCTC ACGCCTGTAA
47651 TCCTAGCACT TTGGGAGGCC GAGGCGGGTG GATCACAAGG TCAGGAGATC
47701 AAGACCATAA CACGGTGAAA CCCTGTCTCT ACTAAAAATG CAAAAAATTA
47751 GCCAGGTGTG GTGGTGGGCG CCTGTAGTCC CAGCTACTCA GGAGGCTGAG
47801 GCAGGAGAAT GGCGTGAACC CAGGAGGCGG AGCTTGCAGT GAGCCGAGAT
47851 CGCGCCACTG CGCTCCAGCC TGGGCGACAG AGCTAGACTC CGTCTCAAAA
47901 AATAAATAAA CCAGAGGTGG GGCCACTTGG GTGACATCCC AGCCCTCTGC
47951 AGGTTTTGTG GGCACCCTGG AGTCCTTGCC CCCTGTGAGG GTCTTGGCCT
48001 CAGCTGGGAT TTACAGGTAG GGCAGCCCTC TCTAACCAAC CCCGAACAGG
48051 TCAGCATCAT TCACTGAGCT AGGTGGGCTT TGCTTCTTGG TGGGAATGAG
48101 AGACAGCAGA GCTCCCGTGA GTTTAGACCC ACCGTCTCAC TACTCCTGGG
48151 CCCCCTCTTC TCTAGCCTGT CGCAGTCTGT GGAGTCTTGT TCAGTGGAGT
48201 CACTTGGTGC CTGGCTTGAG GTTCCATGCC TAGCCCTGGG TTTGGGGATG
48251 TCTGAGCCAT TGACAGCAAG CTGGCGGTGG ACGGCTTCAG GTCTGGTCCA
48301 AGAGGCCTCC AGGCAAGAAG TAGGACAGTC AGGATGCTTT CTGTGTATGT
48351 CCTAGGAGAG AAGACACACA TTCTAGCTGT CGATGTATCA TCTGTGCCCT
48401 GTGCAGGGAT GGTAGCCACA CATTTGTCTC ACTGCCTATT GAAGAACTTG
48451 CAGGCATCAG GCTGCTCCTC AGTGGCCCCC AACCCCACTG GAACTCAGTG
48501 AGATGGAGTA CGCTGGTTAG GGAACTATCA GAGGCAAAGA ACATCACATG
48551 GATATGGCTC CCTGCCCTGG AGATCAGCCT TCTTCCTTTC TTCATCTTC
48601 CCCTTGCCCC TCCCTTGCTG TGCCCCTCCG TGTAATGTTT TTGTTTGTTC
48651 GTTTGCTTTT GGTTTTTTGA GATGGAGTCT TGCTCTGTTG CCCAGGCTGG
48701 AGTGCAGTGG TGCAATCTTG GCTCACTGCA ATCTCTGCCT CCCAGGTTCA
48751 AGCAATTCTC TTGTCTCAGC CTCCCGAGTA GCTGGGATTA CAGGCATGTG
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<center>FIGURE 3P</center>

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48801 CCACCATGCC CGGCTAATTT TTGTATTTTT AGTAGAGACG GGGTTTCACC
48851 ATGTTGGCCA GGCTGGTCTT GAACTCCTGA CCTCAGGTGA TCCACCCGCC
48901 TTGGCCTCCC AAAGTGCTGA GATTACAGGT GTGAGCCACC GTGCCCACCC
48951 ACCCACCATG TAGTTTTGAA AGGCAAGGAG ATATCCCTGG TGGTCATGGT
49001 GCTGTTGGGA ATGTTGGCCT GTGTGTGGCC TACTCTGTCC TGGGGGCTGG
49051 ATTCTGGGAC TACAGCTACA GCCCCGCTGG GTTTCACCTG CCCCTCCCCG
49101 GAACACTGCC CTTCTAGCTG ATCAGGCCTA AGATTTGTCA GACAAAAAGG
49151 TGAACAGCAC AGTCCTGACT CTGCTCCCTG AGGTCAGTGA ATGCATTTTG
49201 TGTCTGAAAG GGACTTCCAC CCCCATCCTC TGGACACCAT CTCTTAGGCC
49251 AGGCATACTT TTCTTTTCTC CTTCCTCTTT GTTTCAGGCT TCGAGCTGGT
49301 GTTGTAAGAA GGAAATACAG GTGCTGGGTT GAAAGTGCAG CAGGAGACTG
49351 CCCACAGATA GGGGACCAGA GTTTCTGAAT TTTGTTCTGC TTTCTTATAA
49401 ACTACCCCCC TTTTTCCTGT ACAGTGGGAA GAAGATCTTG AACTTCTTTG
49451 GGTCAGGTGT GGATTTTGCA ATGACCTGCC ACCTGGCATA AGCAGAGATT
49501 TCTGGAGGGA TGCTTTAAAA CAAGGCTTTG GGCTGGTCCC ACCTTGAGGG
49551 TGCCCCCAGA GCTAGGTCTC TGGGCCCCAC AAATACTTCC TCTGATCATC
49601 TCTCTAGCCA TCGCTCCCAT CTACACAGCG TTATGGAGGC CACCTCAGGC
49651 CTACCTCCTC CAGGCCAGAC CAGGGGGCAA GGGAGGTCTG GGAGTTGAAC
49701 CTGAGTGGCC TTGGGGACTC TGGAGGAACT AAACCATCTG TTTTCTTGTC
49751 TCAGCCACAG AGCAACAACA AAAACAGTCT CGTAAGCCCA GCCCAAGAGC
49801 CCGCGCCCTT GCAGACGGCC ATGGTACCTC CTGACTACAG CTTCTCCGCC
49851 TCTGACCCTG GCTGCCTCCT GCCCCTTCCC TCTTCCTCCT CTTGTGCCCC
49901 CTCCCTGGCC TCCTGGCCTG TTCCTTTCTT GGTCCCCATA GAACTGACTG
49951 CTTTGTGTGC CGCCCTGTAT GCCCCTTCCC CTTCATTGTC CCGCCTGGCC
50001 GCGCTCCATC CCGCATGGCA GAAGTGCTGC TCCTGCTCCT GCTCCTTTCG
50051 CTGGTGGGGG GAAGAGTGAT CAGGGCTCTC AGCTGAACCT CCCAGGCCCA
50101 GCCCAGGACC CCTAGTGGGT CTGCTGTGGG GGCTGGGAAG GTGAGTTGCT
50151 TAGGAAAGGA GAGGGTAGGA GCTTTCTTGG GACCTGAACA TCAGTTCTTG
50201 GAGGCCCCCT TGTAAAACCT GCCTCAGCCT CTCCTTTGCA AAGCCAGAAA
50251 CAGGAAAGAG GGCTGGGGTC CCCACCTCTG GATGGTGCTG AGGTCTCCAG
50301 GCTCCTGGAG TGCCTCATGC TGGCTAAGTT CTCTCTGGGC TCCTCCAGGG
50351 GTTCTGTGTG CTCTTGGAGG TCCCTCTGCT AGTGGTGGCT AACTAGAGAG
50401 TCAGCAGGGG GGTGACTGGG AAAGAGGGAG AGGTGATGTT GCCTGCTACT
50451 CCCCTCCTTG CGGACCCTCA TACCACGTGA CGTGCGCGCG TGGGGCCAGG
50501 AACTAGGGAA GGCAGAAGGC GGGCGCAGTG GGCAGCTCTC TGGGCTCAGC
50551 TTGCTGAGGG GGCTCCTGT CCTGGCTCTT TCTGGGAGAC CTCATTCTTC
50601 TGCCCATGTT CCTGCCTCAC ACATTCCCCG TGATGAACGC TGTGGGCGGG
50651 GCCCGGCCTG TGCCCTCAGT CCCACAGCTC CTCTAGTGTA CCTGCCCCGT
50701 GGGAACCCCA TGTGGAAAGA GCCCTCAGAA CTGACAGGAA TCAGGGACAG
50751 AGGCCCTTGC TGTCAGCCTC CTGGGCACCT GCACCTGCCA GGCCTCTCTT
50801 TCTTACCAGC CCAGTGCTGC TGCCAAAATC CAGGGCTATC CCAGCTGCCC
50851 GGGACCCCAG TTGAGCCGGG ATATTTTGTC TTCTGGAGAT GGCTGGTGGG
50901 CAGGCCTCAG TGGTCATCAT AGGGTCTGCG GGGGTCCTGG GGTGCAGGTG
50951 GGGCTCCTCA GGGAAGAGCC ATAGTCTGTC CCCAAGTCGG AAGGGTAATC
51001 TTCATCTTCT CTCACAGGAG CCACAAACCA CTGTGGTACA CAACGCTACA
51051 GATGGGATCA AGGTGAGTGG CTCCTGAGCC TGCCTCCTGC TTTCCAGGTC
51101 AGCAGGAGAC AGGTGGGCTG GGTCCCAGGG GTCTACAGGC TGCACCCTGA
51151 GGCCAAGGTG TTTGCAGAGG CTCAGCTGAA GGTAGCCTGT GCCCACAGTT
51201 GCTCCATGCT GAGGAAGGGC ATTATACCTT ACAGAGCTCA GGCTTTGCAG
51251 TCAGACAGAC CTGGTCTGAA TCCTGGCCCT GCACCTTAGT ATCCTTTATC
51301 TGCAAATTGG GGATGATAAT AATAGAATCT TCCTCCATAT GTCGGAAGTT
51351 TAAATGAGAG TAAACGTTCA CTGAAAAAAT AGGCAAGAGT ATCTCCAGAC
51401 CCTGGAGCGT TCTCCATGGC CTGACCCCTT TGTGCCCTTG ATGTTTTCAC
51451 CAGCATTCCT GAACATCTGT TAAGCCCAGA TACCATCCAT GGCTCTGGCT
51501 TACAGAGGTG ACAAGACAAA TTATCTGTTC AAACGGTGGG TGGGATGGGA
51551 GGCAGATAAA AAACCAATAA GCAAACAGAT AAGATAAGCT GGGCACCGTG
51601 GCTCACACCT GTAATCCTCA CACTTTGGGA GGCCAAGGTG CGCAGATCGC
51651 CTGAGCTCAG GAGTTAGAGA CCACCTTGGG CAACATGGTG AAACCCTGTC
51701 TCTACTAAAA TACAAAAAAG TAGGCAGGTG TGGTGGCGCG TGCCTGTAGT
51751 CCCAGCTACT TGGGAGGCTG AGGCACGATA ATTGCTTGAG CCTGGGAGGT
51801 GGAGGTTGCA GTGAGCTGAG ATCACGCCAC TGCACTCCAG CTTGGGCTAC
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FIGURE 3Q

```
51851 GCAGTGAGAC TTAATCTCTC AAAAAAAATA AATAAGATAA AATCTAATGT
51901 CAATAGGTAA TCTGAAGAAA ATGGCAGAAA GTAGAGAGAG GGCCAGGTGC
51951 GGTGGCTCAT GCCTGTAATC CTAGCACTTT GGGAGGCCAA GGCGGGCGGA
52001 TCACTTGAGG TCAGGAGTTC AAAACCAGCC TGGCCAACAT GGCAAAACCC
52051 CATCTCTACT AAAGATACAG AAATTACCTG GGATGGTGG CACATGCCTG
52101 TAATCCCAGC TACCTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGGG
52151 AGGCGGAGGT TGCAGTGAGC TGAAATCGTG CCACTGCACT TCAGCCTGGG
52201 CGACAGAGCA AGACTCCATC TAAAAAATGA AAAACAGAAA AACCTCACCA
52251 AACTAGACAG AGAGAACAGG GCCTTGAATT AAGTAGTCAG GAGAGGGCTT
52301 CTTTCAGGAG GTGATATCTG AGCTAGAAAC TGAATGGTAG GTGGGAAGGA
52351 GGCAGCCAGG CCAGCTCTGA GGCTGAGTGC CCTAAGCAGA AGGAACTGAA
52401 GCTCAGATGT GGCCTTTGTA ATCAAGCAGA GGGAAGAGCA AAGTGAGACG
52451 GGGAGAACCA TAGGAGAGTG ATGAGGTTGG AGAAGCAGCA GGGCCTGCTA
52501 CAGAGGCCCT TGTAGGAGTT TGCATTTTCT TCCAGCAGCA AGGAGAAGCT
52551 ATTGGGAGTT CTTAGCAGGA GTAACAGAAT CTAGTTGACA CTTTAAAACA
52601 CCACTCTGGC CTCATGATCA AGAACTCTAG GGAGGCCCGG GCGTGGTGGC
52651 TCACGCCCGT AATCCCTGCA CTTTGGAAGG CCGAGGCGAG TGGATCAGCA
52701 AAGGTCAGGA GCTCGAGACC AGCCTGGCCA ACATGATGAA ACCCCATCTC
52751 TAATAAAAAT ACAAAAATTA GCCAGGCATG GTGGCAGGCA CCTGTAATCC
52801 CAGCTACTCA GGAGGCTGAG ACAGGAGAAT CACTTGAACC CGGGAGGCAG
52851 AGGTTGCAGT GAGCCGAGAT CATGCCATTG CACTCCAGCC TGTGCAACAA
52901 GAGCAAAACT CTGTTTCAAA AAGAAAAAC TCTAGGGAGG AGGTAAGTGT
52951 GGAAGTTAGG GAGACCATGA AGCTGTTATC ATGGTTCAGG TGTGAGATGC
53001 TGGTGGCCTG GAGTCAGGTT GTAGCTGTGC ATTGGAAGTG AAGAGGTAAG
53051 ACATGGGGTT TACTTTGGAG GCAGAACCAG AAGATTTTAT TTTAGATTGG
53101 GCGATCTGAA TATAAGGGAA AAAGAGAAAG AGAAGGATTG AGGATGACTC
53151 CAGGTTTTAG CCTGAGTAAC TGGGTAGATG GTGGCATTTA CCAACTGGGG
53201 GAAGACTAGG GAGGGGATTT GGGAAGAGTC AGACAGCCAG GGTGGAAGCA
53251 GAACCTTCCA CAATTCCTCC TTGCACCTCT TGTAGGAGCA GAAACTCTGC
53301 TTTTGTTCTG CTTTGCTCCT CTGGCTTCCA AGGGATGGAG CATATAGAAA
53351 CATGTTCTTT TTGGCCTACA GGGCTCCACA GAGAGCTGCA ACACCACCAC
53401 AGAAGATGAG GACCTCAAAG GTAGGTGCTG GCCCTTGGAG GGGGAAGGAC
53451 TCCAGCAGTG ACCCAGGTAC CTGGGCTCCA ATGGGGCACC TGCCTTTTCT
53501 GTCCCCAGAA CTGGGAATGC TGGCTCCTAT GCCCCTAGGA GAGGGCTTGG
53551 TATAAAAGCT ACTTTCCACG AGCCAAGATA TGAGGCCCCT GTCTGGTGTT
53601 GCTGAGTTGG GCAAGAGGCT TCTCTTCTTT GACCCCAAGT CTAAAATAGC
53651 TAAGCTAGAG ATTCTCCAGG GGCCAGGGCT CAGAGAACTG TTCCTGTTGC
53701 TGATAATGAT GTGCCATCCA AGAACAGGGG TACCCCAAGT CCCTGCCGAA
53751 GTAGCCTGTA AGTGCTATGA GTCATAAATA GAGTGACCAA TCACTCCTGG
53801 TTTTCCTCGG ACACAGAACT TTTGGTTTTA AGACTGTGAT GGGCCAGGAG
53851 TGCTGGCTCA CACCTGTAAT ACCCAGAACT TTGGGAGGGC CAGGGCAGAA
53901 GGATTGCTTG AGACCAGGAG TTTGAGACAA GCTTGGGCAA CATAGCAAGA
53951 CCTTGTCTCT ATTAAAAAAA AAAAATTAGG AACAAATAAA TAGGCCAGGT
54001 GCGGTGACTC ACACCTGTAA TCCCCACACT TTGGGAGGCC GAGGCAAGTG
54051 GATCACTTGA GGTCAGGAGT TCAAAACCAG CCTGGCCAAC ATGATGAAAC
54101 CCCGTCTCTA CTAAAAATAC AAAAAAAGGC CGGGCGTAGT GGCTCACGCC
54151 TGTAATCCCA ACACTTTGGG AGGCCAAGGT GGGTGGATCA CCTGAAGGTC
54201 AGAAGTTCAA GACCAGCCTG GCCAACATGG TGAAACTCCA TCTCTACTAA
54251 AAATATAAAA AATTAGCCAG GTGTGGGGCA GGTGCCTGTA ATCGTAGCTA
54301 CTCGGGAGGC GGAGGTGGGA GAATCGCTTG AACCTGGGAG GTGGAGGTTG
54351 CAGTGAGCCG AGATCACCCC ATTGCACTCC AGCCTGGGCA ACAAGAGCGA
54401 AACTTCTTCT CAAAAAAAA AAAAAAAAA AAAAATTAG CCGGGTGTGG
54451 TGGCGGGGTC CTGTAATCCC AGCTACTCGG GAGACTGAGG CATGAAAATG
54501 GCTTGAACCC GGGAGGTGGA GGTTGCAGTG AGCTGAGATT GCACCACTGC
54551 ACTCCAGCCT GGGTGACAGA GCGAGACTCT GTCTCAAGAA AAAAAAAAA
54601 AAAAATATAT ATATATATAT ATATATATAT ATATATATAA ATATAAAACC
54651 CAGATAGTCC TGGAACACT GGGATGAGTT GGTCACTCTA GTCTTAAGAT
54701 TTTGGCCTGA ATGATGGAGT TGGAACTAAT CTGACAACCG TGAGGCCACA
54751 TTTGGTCATG TCCTGGTGGG CCCGTAAGGA CCACTAGCCT AAGCITGGGC
54801 CTGGCTAGAG TGCCAGGGCG GTGGGAGGGC ATGGCAGGCT GGACCCCCGG
54851 GAATCTCTGT CCTGCTCTTT GATTGGGCCT CCTGGAATTG CTCCCTTTGC
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FIGURE 3R

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54901 CTGAATTCAG TAAGTGACCT TGGGCCAGGA CATCAGAAAA GACAGAGGAA
54951 CACTCTAGGA CAGAGCTGGG AGAGCATGCC CTGGGTGGCA AGGGGGCACC
55001 AAACCTTTTG GAACCAAAAA AAATAGCAGA AAGCTGCGAG GAAGTGAATC
55051 ATAGTAGCTC CAGGCCCCTG TGAGTGAGGT CAGATCAGTT TTGATTCCGG
55101 CACTGCTGGC AACATAGGAG GCGCTGTCAC TGCTGGGCTC TGGACCCTGT
55151 GGCCTGGCCC CCTGGAACAT CTTCCCCGGG ATCAGGGGTC CTTGGACAGG
55201 CTGTTGTAAG GCTCGTCTGG AAGCCACAGC CCAGGTCTGG GCACCTGCCT
55251 GGTGCCCTCA GCTGGGAGGC CTCTCTGGCA GAGGCGGCGG CGTGGGATGT
55301 CGTCCAGTGT CCACAGCAGC CTGAGGCGAG GCGTCCCCTT GCCCCGGCTC
55351 TACAGCGCCA TGGGCTCGGG GCCTGTCTGG CTTGCTCGCT CACCTGCCTT
55401 GTTCTGTTTG TTTTGGCTGC TCTGCCTTGC CCTGCCCTGC CCTGCCCTGG
55451 CTGGCTAGCT GCCCCGCTCC GCACTGGGAA TGGCAGCTCG GTGCCTGAAG
55501 GACGGAGCTC CCGGGACAGA ACAGCCCCCT CTGCAGGCAT GCAGCCCCAG
55551 CCTTCTCTCT GCTCCTCAGC CAGTAAGTGT GAGGGAGGCA CATTCTGGCT
55601 TCCGTCTCCC TGGCTCGTCC TGAAGCCCCT CAGGGACCCC CACCACAGCT
55651 GTCAGTCCCA CCCACCTGCC CGTGGTAGTA AGCTCTGGGA GCATGGCCTC
55701 TGCTGGGGGT GGGGGGTAGA CTGGAGGTGC TGTTGAGACC AGGCAGGGGC
55751 CCCTGAGTCT GGGGCCCAAA GAAATATGAG AAGTGTGGGT GGAAAAACAT
55801 GGCCTGGGAT GAGGGGAGTA GAAAGCCCCC AGGATGTGCA GTGGGCCTTG
55851 CCTCAGCGCT GAGCCAGGAA GAAGGGCAGA GTCGGAAGTC AGGTCTGTGG
55901 GGGTGGGAGT GGGATGGATGG GGAAATCGTG ACAGCGAGGA ACTGTGTTGG
55951 GGATGTAGTG CTTCCTGAGT CTCAGCATAA CAGTATTAAG AGCATGGGGT
56001 CAGAGGCAAG ATAGATCTGA GTTTAAATCC CAGCTACACT GCCTTCAAGA
56051 GTGTGAAGTT TAACCTCCCA GAGCTGCAGG TTCCTTATCT GTAATGTGGA
56101 AATAAAATGG CACGCACCTC AGAGCCTTGT TAGATAAAAG ACAAGGCAGT
56151 AGGAAGTCTT GATACGGTGC CTCGATGGGT TATCAGTAGC TCATCCTCAT
56201 ATTTCTAGTT ACGTCTGTGC TGGAGGATGC CTTTGTCTGC TGCTTTTCCT
56251 CCCACCATCT ATCCTTGCAG AGTTTCTAAG CACAACCCTC TTCGCCCGTG
56301 GGGCCCCAGT CAGGTCATCC AGATGGGTCT GGTGGGGTTG GAGAGGGTGT
56351 GTGTGTTGTG GGTGCACACC TGCCTGCTGC TTTTGGAAGC CGATCGAACT
56401 CCTTGCTTCC CTTAACCTGC TGCTTGCTCA CCTGGAGCTG TGGCCTAGCG
56451 GGGCTGACGG CTGTGGGGCC CCCTCCTGGA TGTGCCTTTG GCTGCGCTGC
56501 CCTGTCCCAA CTGTGCTGCT TGGCTGTGCT GGCCCGGCTG GGCCGTGGTG
56551 GTGCTGTTCT AACGCTTGCA GTTGTCTTGC AGCCTTTTGC TCCTGTGAGG
56601 AAAGGGTTGT GGCCTGGCCC CGCCCAGGGC TCGGGTTAGG ATGAGCCCAA
56651 GCTCAACCCA AGCTCTCCCT TACCCTGGTG GCAGCCCCTG CTGGTAGTGG
56701 CATTCCCTAT AAGAGAAGCC CATGCCGGCA GGACATCACC AGCTGTCCCT
56751 TGGCTTTGGA TGGGTTGGGG AGGAGGCCTC TGGAGGGCAC CACCTCTGCC
56801 TGCCTGTCAG TCTGAGCCCT GTCTGGTTTT CCTGAGGAAC ACGTCCTGGC
56851 AATGAGAGCT GGTGTGAAAT GTGCAGCTTT CCCAAGCCTC GAGAGGTAAA
56901 TGGAGCAGCC TCTCTGGTAC AGGCTGTCCC AAGTTTTTAC AGTTCTGGGA
56951 TCATTTCTCC CAGAAAAGCC CTGTGGAGTT GAGCAGTGGG AAGCATCCAT
57001 CCTAGGGTTC TGATGGTCTT TTGGCACCCC AGCCCTAGCT GGATTCTGCT
57051 GTCAGGCTAC CTGTCACCCA GGGCTGGGTC CTGGCCACTG AATGAGGGCT
57101 ACGAGTGGGG GTGGTGATTG AGACCTGACT GAGCCCCTTC AGGTGAGAGA
57151 AGTAAATTGG GGGTGGAAGC GGCCTTATTG GGAGATGCTT GTGAGAGAGG
57201 CTGCTCATAC AGGGGAGGGG CTCACAGCAT TCACGATGTA CCAGGCTCCT
57251 CACCTGTTAA AGGCAAGCGT GTTTTCTGCA ACCTGGTTGT TGATGGAAAG
57301 GGAGGCAAAG GCCAAAGAAC CATAACTAAT GGCTGGGCTT CAGGAGAAAG
57351 TGGTCATTGT CTCTGCAGCA TGCAGAGAGG GAGACGGGAG GGAAGGTGTG
57401 TTCGCTCTTC CTGCCAAGGG CCCTAGAGAC AGAGAAGAGG GATGTCTTTG
57451 TCATAAGCGA TCACAGGGGA CTCCTGAGGA CTGGGGAGGG CTCTCTGTAA
57501 CTTGGGAGGT TCCCCAGTAG GTAAATTGAT GGATTTTTCT CCCCCACAGT
57551 GCGAAAACAG GAGATCATTA AGATTACAGA ACAGCTGATT GAAGCCATCA
57601 ACAATGGGGA CTTTGAGGCC TACACGTAAG TAGAGACCCA TTTTTTTTTG
57651 TGACCTAAGT CATCTCCCAA GGGCTTCCCT GCTTCCAGAC AACAATTAGG
57701 ACCCTGGGGA AAGGGAGGTT GGACCTTGGG CAAAGTATCT GAGTTAAGCC
57751 CTCTCCTAAA CTGGGAGCCC TTCCAGGTAG ATTCCCTGAG CTCACCCATG
57801 GTATCCTGGC AGTGGGCCGA AAGCACAGGG CTGAGTGGCC CAGCAGGCAG
57851 GCCTGGAAGA TCTTTGCTGT CTTGTCTGGC ATGGCCACAG GTAGCCTGCT
57901 GCTACTGGAT AGACACCGCT GATAAGGAAG GAAGACAAGT CACTCCATAG
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FIGURE 3S

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57951 AAGCCTGATA GGCTGCTTTT TTTTTTCTCC CTGTAGGAAG ATTTGTGATC
58001 CAGGCCTCAC TTCCTTTGAG CCTGAGGCCC TTGGTAACCT CGTGGAGGGG
58051 ATGGATTTCC ATAAGTTTTA CTTTGAGAAT CGTGAGTGGG TTCGTGCTGC
58101 TGATATACTC CTGCCTGCCC CTTTACCCCT TTGTCTCTGT CTCCTGCTCA
58151 CCTTCTCATC CCAGTTGCCC ACTTTTCCCT TATTTGACCT TCGTGCTGCA
58201 CTCCTACTCT GTATGCTTGT CCCCTTGTGC CCCGATGGTT GTAGACAGGC
58251 ACCTTTGAAG GCCCTGCTCC TGAGCTCCAA GTGCCATTCA TTCTGCAGCT
58301 GCTTTGTGGC AGTGCCAGTC ACCACAATCA AGCTCACTTA TTTCTTGCCG
58351 GGCGCGGTGG CTTACGCCTG TAATCCCAAC ACTTTGGGAG GCTGAGGCTG
58401 GCGGATCACG AGGTCAGGAG ATCGAGGCCA TCCTGGCTAA CACGGTGAAA
58451 CCCCATCTCT ACTAAAAATA CAAAAAATTA GCCGGGCTTG GTGGCAGTGC
58501 CTGTAGTCCC AGCTACTCGG GTGGCTGAGG CAGGAGAATG ATGTGAACCT
58551 GGGAGGCAGA GCTTGCAGTG AGCCAAGATC AGGCCACTGC ACTCCAGCCT
58601 GGGCAACAGA GCAAGACTCC ATCTCAAAAA AAAAGAAAAA ATTATTTAAG
58651 CCTCACCTCT TTCCAAGACG GATTGGAAGG AAACCCTTTG AGATTAGGTT
58701 GAGATGATCT CAGCACATAA GAACTAAGCT CTGTGTCTGC AGGTTTCACA
58751 ATAGAGGAAA TTAAAACCAG GATAAGAATG TGCAAACCAG GGCACTGTTG
58801 GTGATTTGCG AGATCGGAAG TTGTGGCTAG AATCTTCCTG ACTATGGAGG
58851 AAGGCAGACG TCTTGTATAG GGGGTGGGGT GTACATTCTG GACAGTTCGT
58901 GGAAAATAAG GGGATAAGAA GCTGAATCAT CACCCCCTCC CATCTTTCTC
58951 TCTGCTCTAT GAGACCCTCC CCTTCCTTAT TTTTATCTCT TCCCACTTTA
59001 TGCTGGGCCT TCCCTATCCT GCCCTGAGTT ATAGTTAGTC ACTAACTTCT
59051 CCGCTGGCTC CCACCCTTAT CACATCTCAG CTACATATAT AAACTCTCTG
59101 TTATCTAAGT AATTCTATTA GCCAGAAGCA ATTCCAGAGT TTATATTAGT
59151 ACTAGGAAGG TGTCATGTAG CCCCTGTCTA ACATTTGAAT TGAACTAAAA
59201 TGTGAATCTC AATAAAAGCA ACACAGTTTT CACAGCATAT GCTGATAATG
59251 GCAATCCAAC TTCTTTTGCC TTTTCCCCAG AGAATCCTGG GAATATCCTG
59301 AGCTTGGTGC TTTGATGATT CTATTTCAGC TTTGGTGCCT TAAAAAAAAT
59351 TACAAATCAA TTTTGAATGG TTTAAGTTCA TGATTTTGTT CTGCAGCCCT
59401 AGCTAGGGGT GAGCCAAGCC TTATGAAATC TAAACTCAGC CTAACAGAAT
59451 AGAAAATCTA TAGGCTTTAG TTAAGAGTCA CATGGTCCTG AGTTCAGGTG
59501 TGTGATTTGA GCAAATTATT CCTTGAGCCT ATTTCCTCAT CTTATAATGA
59551 AGAAAATATT ATCCACCAAG AAATACAGCT CGGGCATGTA AAACCCCAGC
59601 ACAATGCCTG ATTAAAAGCG CAGCAGGTAC TGTCACTGTT ACCCATCTTT
59651 CTGTTCCTTT TGGATAAAGG AGACTAATGT AATGTGGCAT CCTGGCCTCT
59701 GGAGGGCGTT CAGGGGTTCG GGGGTGGGGG GGGGCGGTAC TTGGAGATTC
59751 TGGGAGTGGT TGCTTGGGAG ATGGTAAGAC TTGGAAGTGC AGGCTGGGAG
59801 GAAAATGCAG GTGCCCAGGC CTGATGTCCT CTTACCTACC CCACCCTGCC
59851 CTGCAGTCCT GTCCAAGAAC AGCAAGCCTA TCCATACCAC CATCCTAAAC
59901 CCACACGTCC ACGTGATTGG GGAGGACGCA GCGTGCATCG CCTACATCCG
59951 CCTCACCCAG TACATCGACG GGCAGGGTCG GCCTCGCACC AGCCAGTCAG
60001 AAGAGACCCG GGTCTGGCAC CGTCGGGATG GCAAGTGGCT CAATGTCCAC
60051 TATCACTGCT CAGGGGCCCC TGCCGCACCG CTGCAGTGAG CTCAGCCACA
60101 GGTGCACCTG GTTGACGGGG GAGAGGGGCT GGAAGGGCCT GGGATAGGTG
60151 GGGTCAGAGG AAGAAGAGAA GGCTGGGAGG TGGTCCTGGG AGAGGAGGTG
60201 TGGGCCGTCC CAGAGGACTG GCAAAGCCTG GCAGAATGGT TGCAATAAGT
60251 TATGCTTGGA AATCAGACAG ACTAGGGTCT GGCTCCGTGA CTCCAAATTG
60301 GATGACCTCA GACAGGTTAC TTCCCCTCCC TAAACTGTTT CCTTAGCTGT
60351 CAAAGAAAGG CAGAGAGTGG TGCCTACCTC ATTTAATCAT TGTGAGGATT
60401 AAGTAAGATA CTATAAGTAA AGCACTTAGT TAGTGCTTAG CAAATGGGAG
60451 GCAGTTTTGT ATTTAAGCAT TAGCTTCACC CACTTTCCCC ACCTTCTCAG
60501 GCCGACTTGG CCATGTGTTT AGCGTGCTAA AGTCGCTGGA ACTCATCTGT
60551 GTGCTCATTG TCCTCTGTTC TGTTACCACA TTCTGTCCTG TTTGACAGGG
60601 GCTTTAGGAG ATTCCAGCCG GAGGTCCAAC CTTCGCAGCC AGTGGCTCTG
60651 GAGGGCCTGA GTGACAGCGG CAGTCCTGTT TGTTTGAGGT TTAAAACAAT
60701 TCAATTACAA AAGCGGCAGC AGCCAATGCA CGCCCCTGCA TGCAGCCCTC
60751 CCGCCCGCCC TTCGTGTCTG TCTCTGCTGT ACCGAGGTGT TTTTTACATT
60801 TAAGAAAAAA AAAAAGAAA AAAGATTGT TTAAAAAAAA AAGGAATCCA
60851 TACCATGATG CGTTTTAAAA CCACCGACAG CCCTTGGGTT GGCAAGAAGG
60901 CAGGAGTATG TATGAGGTCC ATCCTGCCAT GAGCAGTGGC TCACCCACCG
60951 GCCTTGAAGA GGTGAGCTTG GCCTCTCTGG TCCCCATGGA CTTAGGGGGA
```

FIGURE 3T

```
61001 CCAGGCAAGA ACTCTGACAG AGCTTTGGGG GCCGTGATGT GATTGCAGCT
61051 CCTGAGGTGG CCTGCTTACC CCAGGTCTAG GAATGAACTT CTTTGGAACT
61101 TGCATAGGCG CCTAGAATGG GGCTGATGAG AACATCGTGA CCATCAGACC
61151 TACTTGGGAG AGAACGCAGA GCTCCCAGCC TGCTGTGGAG GCAGCTGAGA
61201 AGTGGTGGCC TCAGGACTGA GAGCCCGGAC GTTGCTGTAC TGTCTTGTTT
61251 AGTGTAGAAG GGAAGAGAAT TGGTGCTGCA GAAGTGTACC CGCCATGAAG
61301 CCGATGAGAA ACCTCGTGTT AGTCTGACAT GCACTCACTC ATCCATTTCT
61351 ATAGGATGCA CAATGCATGT GGGCCCTAAT ATTGAGGCCT TATCCCTGCA
61401 GCTAGGAGGG GGAGGGGTTG TTGCTGCTTT GCTTCGTGTT TTCTTCTAAC
61451 CTGGCAAGGA GAGAGCCAGG CCCTGGTCAG GGCTCCCGTG CCGCCTTTGG
61501 CGGTTCTGTT TCTGTGCTGA TCTGGACCAT CTTTGTCTTG CCTTTTCACG
61551 GTAGTGGTCC CCATGCTGAC CCTCATCTGG GCCTGGGCCC TCTGCCAAGT
61601 GCCCCTGTGG GATGGGAGGA GTGAGGCAGT GGGAGAAGAG GTGGTGGTCG
61651 TTTCTATGCA TTCAGGCTGC CTTTGGGGCT GCCTCCCTTC TTATTCTTCC
61701 TTGCTGCACG TCCATCTCTT TTCCTGTCTT TGAGATTGAC CTGACTGCTC
61751 TGGCAAGAAG AAGAGGTGTC CTTACAGAGG CCTCTTTACT GACCAACTGA
61801 AGTATAGACT TACTGCTGGA CAATCTGCAT GGGCATCACC CCTCCCCGCA
61851 TGTAACCCAA AAGAGGTGTC CAGAGCCAAG GCTTCTACCT TCATTGTCCC
61901 TCTCTGTGCT CAAGGAGTTC CATTCCAGGA GGAAGAGATC TATACCCTAA
61951 GCAGATAGCA AAGAAGATAA TGGAGGAGCA ATTGGTCATG GCCTTGGTTT
62001 CCCTCAAAAC AACGCTGCAG ATTTATCTGC ACAAACATCT CCACTTTTGG
62051 GGGAAAGGTG GGTAGATTCC AGTTCCCTGG ACTACCTTCA GGAGGCACGA
62101 GAGCTGGGAG AAGAGGCAAA GCTACAGGTT TACTTGGGAG CCAGCTGAGA
62151 AGAGAGCAGA CTCACAGGTG CTGGTGCTTG GATTTAGCCA GGCTCCTCCG
62201 AGCACCTCAT GCATGTCCCA GCCCCTGGGC CCTAGCCCTT TCCTGCCCTG
62251 CAGTCTGCAG TGCCAGCACG CAAATCCCTT CACCACAGGG TTTCGTTTTG
62301 CTGGCTTGAA GACAAATGGT CTTAGAATTC ATTGAGACCC ATAGCTTCAT
62351 ATGGCTGCTC CAGCCCCACT TCTTAGCATT CTTACTCCTC TTCTGGGGCT
62401 AATGTCAGCA TCTATAGACA ATAGACTATT AAAAAATCAC CTTTTAAACA
62451 AGAAACGGAA GGCATTTGAT GCAGAATTTT TGCATGACAA CATAGAAATA
62501 ATTTAAAAAT AGTGTTTGTT CTGAATGTTG GTAGACCCTT CATAGCTTTG
62551 TTACAATGAA ACCTTGAACT GAAAATATTT AATAAAATAA CCTTTAAACA
62601 GTCCATTGTG TTACTGCTGT TGGAGGTTTA CGGCCAGAGG CGTAGATTTT
62651 AGCAGCCTGG GTTACCAGGT TGGAGAGAGT ACCTCCTCCT ACTCCCTTTG
62701 GGTACTTTTG AGAATAAAAC TTCCTCATGC CTGTAATCCC AGTACTTTGG
62751 GAGGCCGAGG CGGGCGAATC ACGAGGTCAG GAGTTCGAGA CCAGCCTGGC
62801 TAAT   (SEQ ID NO:3)
```

FEATURES:
Exon:	1690-1694
Intron:	1695-2000
Exon:	2001-2095
Intron:	2096-14208
Exon:	14209-14268
Intron:	14269-21854
Exon:	21855-21909
Intron:	21910-22781
Exon:	22782-22847
Intron:	22848-25768
Exon:	25769-25841
Intron:	25842-25986
Exon:	25987-26089
Intron:	26090-26492
Exon:	26493-26576
Intron:	26577-27019
Exon:	27020-27114
Intron:	27115-27753
Exon:	27754-27876
Intron:	27877-32559

FIGURE 3U

Exon:	32560-32643
Intron:	32644-32889
Exon:	32890-32932
Intron:	32933-35499
Exon:	35500-35562
Intron:	35563-37589
Exon:	37590-37633
Intron:	37634-46979
Exon:	46980-47012
Intron:	47013-51017
Exon:	51018-51062
Intron:	51063-53371
Exon:	53372-53420
Intron:	53421-55458
Exon:	55459-55572
Intron:	55573-57549
Exon:	57550-57625
Intron:	57626-57986
Exon:	57987-58081
Intron:	58082-59856
Exon:	59857-60086

CHROMOSOME MAP POSITION:
Chromosome 10

ALLELIC VARIANTS (SNPs):
DNA

Position	Major	Minor	Domain
1603	G	A	Beyond ORF(5')
8632	T	–	Intron
19366	G	A	Intron
23770	T	C	Intron
31013	A	T G	Intron
33206	T	A	Intron
33263	G	A	Intron
33859	C	A	Intron
37254	T	C	Intron
40809	C	A	Intron
41025	T	C	Intron
42232	T	C	Intron
50477	G	A	Intron
55352	A	G	Intron
55914	A	G	Intron
56633	G	A	Intron

Context:

DNA

Position	
1603	ACCCCCACCCGCGGCGCCGGAGCCCGGCCACTGCAGCCCCGGCCCCGGCCCGCCCCCCCAGA CGTTTCCAGAGCTCAGAGTGCGAGCTCCCGTTTGACGGGGACGTCAAGGAAAATAGCATG GGAAGGGGAGTTCTTGATGTCTGACTGTGTGTCCTCTCTTCCCTTGCTGTCAGTTGAGCCGG GATGCAGTGAGATGAAACCGGCTGTGGGGGGGTTTGAGCCTCACTTTGCCCCCATGGTTGA GGGAGATTTCTCTTTCAGGGGATGATACCCTCTTTTTAATCTTTCCTTCCCCGACCTTCA [G,A] CTGTTCCTGCTGAGAGAAGGGCAGGGTCTCTCTGCTCCCTTCTGCCCTGGTTCTCTTGGC CGGGACCGCAGGGCTGTCTGAGATGCAGCAGGTGTGTGTTTTCAGCATCGCCCACCCGCT CCTGATGTGCAGCCTGAGGTGGAGGCTGTTGCCTTGCCCAGGGACTGGATGAGGGGGTGG GAGCGCGGCACGCCACCCACATCTGTTCAGTGTCCTGCGGTGGCCGCGTCCTTTTGCCTC

FIGURE 3V

ATGTTGGATGGTGGTGGTCACAGCGCCGGTGTGTGTGTGCATGTACGTGAGTGTGACTAGAG   (SEQ ID NO:5)

8632   GACGGCGGCCTCTGCTGCTTGGGAAGAAGATGAAAGGCACTCAGGAGGGCAGCAAGTGAG
GCCGCCTCCCATGGAGCCCTGAAATCAGTGGGGTTGCAGGAAGTTTCTCACATCCATGTT
TAGGGTCATAGGCACAGACCTGCAAAATACCCTTTGCAAAGTTAAGAATGTCTTTGAGAT
TGGAACTTGGGAGAGTCCTCAGTCAGAGTAGGAATGTGCATCCTTTCCCACGTACAGAGG
ATTGTATGTTTACGTGGCAGCAGGATCTTATTTGAAGCTAGTGCTGGCATTTGTGTTTTT
[T,-]
TTTTAGGAAAATGTCACTAAGTCAAGCAGGCCCATCCCTGAGAGGGCCATGGAGAATCTG
TGGCCAGCCCTCCCTGGCCCCCTGACCTGGCAGAGGAAGGAAAGGGCATTGGAGTAGGCT
TCTGTCTTCAGGCCAGAGGGGGAGGTGGTTCAGGGGCAGGCTTGGTGCACCCCTTGGCTG
CAAGCTATCACCTCCCTATCTGCTTCCTCTTTTCTGCCTCCCCTGGTGCATCTGGTCACT
TCTTGCTGCCCTTCCTGTGAAATCGTGGCACCTTGGACCAAGTCCTGAAGCACTTGGGCA   (SEQ ID NO:6)

19366   CTCAGGAGGCTGAGACAGGAGATGGCTCAAGACCAGGATCTCCAGCCCAGCCTGGGCAAC
ATAGTGAGACCCTGTCTCTTAAAAAAAAAAAGAAATAATGAATCTGCTGTTGCTAAATAG
GCACTTAGAATGGCACAGTCATTTCTCCTCTTGTCTTCAGTGTCCTGTTAATTTCTTTAC
AAATTAAAAAAAATGTCGATAGCAGTCTTATTCAGATACAGCTTCCTCCATCCCTCCTTGT
CTTGGCAGGTGCCTTGCTCTGGGGCACACATCAAAGCTGTTCTCTCTGCTGGGTGGCCTA
[G,A]
AAGGATTAGTCTTCCTTTGCTGCTCCTTTCTTCTAATTCCCTTCCCCGGCTTCCTCCCAC
CTGGGCTCTGTGTGTGGCCTTCCTGGAGAAGGGCAGACGCCAATGACTCCATGTCTAGGC
AGAGGCCTGGGTGCCTGCACTTCTTGCCCTGTTCTTGGCCTTGCTGTGCTGGCGGGGGC
AGGGTGGTGTGGGCATGGGGTGGTGTTGGGCATGGGGTGGGGTTCTGGCTGAGGCAGGG
CTCAGTGCCAGGCCCAGGCAGAGCTGAGTGGCTCCACTTCTCTGAGATGGTTGTCAGCAT   (SEQ ID NO:7)

23770   CCCCCTCTGCCCTTTTCTTTCCTTTGACAAATTCTGGTGTGCTCAAGCCACTGTGCTGAG
GCTCTGGCATGATCCAGAGGTGCAGAAGACATGGTTTCTGTCCTGAGGGAGTGGAGAGTT
CTGGGCTGATAATCCAACCATAGAGCCCCGGGAGCTTTCAGCCTCTGTCACCTTGTCCCT
AGACCACCATGACCAGCCTTGCCGTGGGGCTCCTCCAACTTGAGGACCGTTCCCCGGCCA
CATGCCTCAGCCTCTGCCCCTCCCTGGAATCCCTGGTGCCTCCCTCACCCACGCTCTCAGG
[T,C]
GCCTGTTCAGCCTGCCTTTCCCGGCCTTGGCTCTTCCCCCAGCCTTGCTTTTCTCGAGGGT
GATGTCCCTACAACCTGGTTTTGATCATCCTGCCTGCAGCCTTATCTGGCTTATGTGGCAG
CTCTGGCTGCTTCTGGAGAGTGGGGGAGTGCAGCTTCCTCACGAATTTCTCAACCTTGAG
AGGCCAATGTTTGCTGATCAACTTCAGATGCTTCAGCCTCGGGAAGAATTCTCAAGTGGG
GAGATGAATTCCAGTGCCAGCAGGGGAGGACGAGGCTCTGGGACGGAGGAGGCAGTGATG   (SEQ ID NO:8)

31013   TCAGGAGCGGTGGCTCACACCTGTAGTCCCAGCACTTTGGGAGACCAGGGTAGGTAGATC
ACTTGAGCCCGGAAGTTTGAGACCAGCCTGGGCAACATGGCAAAACCCCATCTCTACAAA
AAAAAAAACTTTAAAAATTAGCTGGTTGTGTGGTAACGTGCCTTAGCTACTTGGGAGGCTGA
GATGAGAGGATCACCTGAGCCTAGAGAGGTGGAGGTTGCAGTAAGCCATTATTGTGCTAC
TGCACTCCAGCCTGGGCAACAGAGTGAGATGCTGTTTCAAAAAAAAAAAAAAAAAATTTTTTT
[A,T,G]
TTTAAGGAGAGGCTTAACTATAATCTATAGAGAAGAATCTAGTCCAGAGGAAAGAGTTGA
AGATCCTTGCTAATTGAGGAAGCAAAGGTTTGGACAGCAGAAAAAGAGAGGGGGCTCCTG
AGCCAAGGGCAGGGGGTCCATCCCGGGGATGACCATGATCCCCCTGAGACTTCTATTAGT
GTGGAGGCAGGTGAAGATCGGCTTGTGAGTGGAAGTCTGAGCTGAAAGGGGTTCTTGCTG
ATGACCTCTCATTTTGCTTTTGGAGAAATTTACACCGAGGAGGAGGTAAAATGAGAGACT   (SEQ ID NO:9)

33206   CCATGCTTGTCTCCAGGAACTTCTCAGGTATGTTTTCCCAGCTGTGTGTACTTTGATTATGC
CGAGGTGAGTGGATCAGGAATGGGCTGTTGCCATCCCGGGCACCGCTGGGTTTCCTCGGC
GTCCTGGGCCACACCTTGACCAGGGCGAGTGAGGATCCTGTTTTGAGGGGCTGCTGCTGC
TGCTGAGTCCTGCTCCTGAGATTCAGGGGGCTGGACTCACATTTGTGAATTGTTCCTAG
AACTTCCCAAGGAGTAGCCTGCCCAACTTGCTATGTACCTTGTTTCTCTGGATTCTTATT
[T,A]
AACTCTCTGAAGACTCTCAGCCACTTTACAGATTTTAGCCATTCTAGGATCTTGGAGGATG
TGCTGGGGGAAGAAAAGAGAGATGAGGTACAGTGAGTCTTCTCAATTGCCAAATTGCCAC
CATTCATTTGCCTGCTGGGACGATCTCTTACTTCATTTTGTCCAAGTGGAGATGACTAAT
AGAAATTATTCCAGATGTTTAAACCTTTTGTGGCGACTTGTGCTTAAAATAGTCCCTGAG
ATACTAGCTATAACAGTGAAGAAATAAAGACCAGCAGGAGAGAGGGAAAGGAACTTGCTT   (SEQ ID NO:10)

FIGURE 3W

33263   TGCCGAGGTGAGTGGATCAGGAATGGGCTGTTGCCATCCCGGGCACCGCTGGGTTTCCTC
GGCGTCCTGGGCCACACCTTGACCAGGGCGAGTGAGGATCCTGTTTTGAGGGGCTGCTGC
TGCTGCTGAGTCCTGCTCCTGAGATTCAGGGGGCTGGACTCACATTTGTGAATTGTTTCC
TAGAACTTCCCAAGGAGTAGCCTGCCCAACTTGCTATGTACCTTGTTTCTCTGGATTCTT
ATTTAACTCTCTGAAGACTCTCAGCACTTTACAGATTTTAGCCATTCTAGGATCTTGGAG
[G,A]
ATGTGCTGGGGGAAGAAAAGAGAGATGAGGTACAGTGAGTCTTCTCAATTGCCAAAATTGC
CACCATTCATTTGCCTGCTGGGACGATCTCTTACTTCATTTTGTCCAAGTGGAGATGACT
AATAGAAATTATTCCAGATGTTTAAACCTTTTGTGGCGACTTGTGCTTAAAATAGTCCCT
GAGATACTAGCTATAACAGTGAAGAAATAAAGACCAGCAGGAGAGAGGGAAAGGAACTTG
CTTAAATTTGCATAAAGAATTGGGAGAGGTGGGACCAATAATTTGTAAATCATACTTGAC   (SEQ ID NO:11)

33859   TTGACATTTATTTTTAAGATGCAAGACACTCCACTCCCCTCTTGCCCCCACCCTCACCCC
AACCCCTATTATTGTTTGCCTTCAATTGGGAAGCACAGTGGCTTTTTTGTGAGGAAAAGA
TTAATGTCGAGACTGAAGACAGAGAGGGCTCTGCCCAGCTTGCCATCTCCCCCGGTCCTC
CCTCCCTCTAACCCCTTGCCTCACTGTTTTGGTTCAAGACCCCCCCTTCTCCTTCCCATA
ATAAGACTCCCTCCCTTGCTTCCCCTCTGCACCACCATGGAAAGGGGGTTGTGTGGGAGC
[C,A]
TAAGCCACCACTCAGTGGGAGCCACTTCTGAATACCCGTCCTGCTGGGCTCGCCTGCGCT
GGCTCCAGGTAACGCCAGGGCCTTGGCTGTGAGGATGCTGCAGGCAGGGAGCCTAGGGCT
TCGTGGTGTAGCCTGAGAGCCATGGAGCTCCGGAAGGCCAGGGCTGGATAGTGAGCCCGG
GGCTGGTGGTGCCCTGCCCTAGGCCTTCTCCTTTGACCCTGGTTTGGGGCTTGATCTTGT
GTCATGGGTACCCACGACGGGCATACTGTGGTGTGGCTCCACCTCTCGCAGATGGGAACA   (SEQ ID NO:12)

37254   CATTATTCTGCCGAGTCCTTCCTGCTCACAGGTCCAGAGAGTGGACACTGGGGAAAGGGT
GGCAGCTAGGACCCAGTGAACCTGGTGAGGACCTGCTCAGTGAAGGCTTCAACCCCCTGG
CAAAACCCTCCTGTAGGTGGTCCTGGTTTCTGTGTCTGTGTCTGTCTGTCCTCTGGTCTC
CTGTGTGAACTGTGACACTCTGCTTCTTGAGAACACTCAGGAGATGTCTTGCATCCTTGC
AGTTTGGCCATCCAGAGAACTTCCATGGCACCTAGGGATGGAGCCCTCACTCTTTCACCC
[T,C]
GGCACTCTGCTTCCAGGCCTGGGTGGAAGCTGTCAAAGGCAGAGTCCCCAGTGCCCCAGG
CGGCTCCAGTACTGAGCATGGTTTCTCCTCTAAGTGTCGTGCATCCATGCCCTCCTCCAC
GCAGAGGAGATCCTGAGGTGCCACCCTGAGGGCTCTGACGCCACTCAAGATCCCCTTCTT
GCTGAGAGGCTATAGGAAGTGCCTCTTTTGGGGGTTTCGGGAGACCCTTGGCCCCCCTTGT
CAGACACAGCACTCTCTTGTGGATCTGGCTGCCGGACTTCAGGTTGGGGAGAGGGTACAA   (SEQ ID NO:13)

40809   GTCGGCAAAGGAAACAGAGGAAGGACAGAGAGGTAGGGGGAAAAGAGAAATGTGCAGCAG
CTGCAGCTCTTCCAGGAACCCTGAGGATGAGGGCTGGGCAGACACATCATTAGGTAAAGG
CTTTAAATGAGGACGTGCGTGGGGAACCTAGCCCTGCAATGTGTTGTGTGTCTGACCCTG
ATATGTGCTCAGTAAATGAGTTTTATGCCACATTCTTTTGAGAAAAGAGCTTCAATATCA
TGGTGGGAACCAGAGGCCAATGATCACCCAAAATTAAAAGGCCAACCGCGTATTCGCAGC
[C,A]
GTTGTGATGGGAGGGGTTAATATTTTTATTGAAAGAGTTTCTGTGTGACAAATAATCCCTCT
TAAAACCCAGTAGAAGCTGGGCGTGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGG
CCGAGGCGGGTGGATCACGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAAC
CCCATCTCTACTGAAAATACAAAAAATTAGCCGGGTGTGGTGGCAGGCGCCTGTAGTCCC
AGCTACTTGGGAGGTTGAGGCAGGAGAATGGCGTGAACCCGGGAGGCGGAGCTTGCAGTG   (SEQ ID NO:14)

41025   TTTGAGAAAAGAGCTTCAATATCATGGTGGGAACCAGAGGCCAATGATCACCCAAAATTA
AAAGGCCAACCGCGTATTCGCAGCCGTTGTGATGGGAGGGGTTAATATTTTTATTGAAAG
AGTTTCTGTGACAAATAATCCCTCTTAAAACCCAGTAGAAGCTGGGCGTGGTGGCTCACG
CCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGGTCAGGAGATCGAG
ACCATCCTGGCTAACACGGTGAAACCCCATCTCTACTGAAAATACAAAAAATTAGCCGGG
[T,C]
GTGGTGGCAGGCGCCTGTAGTCCCAGCTACTTGGGAGGTTGAGGCAGGAGAATGGCGTGA
ACCCGGGAGGCGGAGCTTGCAGTGAGCTGAGATTGTGCCACTGCACTCCATCCTGGGTGA
CAGAGCAAGACTCCGTCTCAAAAAAAAAAAAAAAAAAAAAAAAAAAACCCAGTAGATAGGC
TAGGTGTGGTGGCTCACATCTGTAATCCCAGCACTTTGGGATGCTGAGGTGGGCTGATCA
CTTGAGGCCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCCCCTCTCTACTAAA   (SEQ ID NO:15)

FIGURE 3X

42232   GGAAACGTAGTGAGACCCCATCTCTTAAAAAAAAAAAAAAAAAAATTAGCTGAGTGTGGTGG
AACGTGCCTGTAGTCCCAGCTACTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGG
AGGCTGAGGTTACAGCCAGGATCACACCACTGCGCTCCAGCCTGGGTGACAGAGTGAGGC
TCTGTTTAAAAAAAAAAAAAAAAAGAGAGAGAAGAAAAAAAAGATTGGAGACAATTTGAAA
AGCCAGTAAGGAGCCAGACACAGTGGTGCGTACCTATAGTCCCAGCTACTCAGGAGGCTG
[T,C]
CGCAGGACAGAATTGCTTGAGCCCAGGAATTCGAGGCCAGCTGGGCAACATAGTGAGACC
CCCAACTCTTAAAAATGTTTTTAAATTTAAAAATAAAAAGATTTTTTAAAAGCCAGTAAA
TGACTAAATAATTATGGGAAATCTACTTAATAAACTATTCAAAAGTTATTAATTTTCATG
ACCGTAGGGATATTTTAAGTGAAAAATAAAGTGCAGAAATGTTTTATATTAAGTGAAGGA
AGTGGTATATAAAGGAGTACAGACAAGCCAGGCACGGTGGCTCACGCCTGTAATCCCAGC   (SEQ ID NO:16)

50477   TTGGGACCTGAACATCAGTTCTTGGAGGCCCCCTTGTAAAACCTGCCTCAGCCTCTCCTT
TGCAAAGCCAGAAACAGGAAAGAGGGCTGGGGTCCCACCTCTGGATGGTGCTGAGGTCT
CCAGGCTCCTGGAGTGCCTCATGCTGGCTAAGTTCTCTCTGGGCTCCTCCAGGGGTTCTG
TGTGCTCTTGGAGGTCCCTCTGCTAGTGGTGGCTAACTAGAGAGTCAGCAGGGGGGTGAC
TGGGAAAGAGGGAGAGGTGATGTTGCCTGCTACTCCCCTCCTTGCGGACCCTCATACCAC
[G,A]
TGACGTGGCGGCGTGGGCCAGGAACTAGGGAAGGCAGAAGGCGGGCGCAGTGGGCAGCT
CTCTGGGCTCAGCTTGCTGAGGGGGCCTCCTGTCCTGGCTCTTTCTGGGAGACCTCATTC
TTCTGCCCATGTTCCTGCCTCACACATTCCCCGTGATGAACGCTGTGGGCGGGCCCGGC
CTGTGCCCTCAGTCCCACAGCTCCTCTAGTGTACCTGCCCCGTGGGAACCCCATGTGGAA
AGAGCCCTCAGAACTGACAGGAATCAGGGACAGAGGCCCTTGCTGTCAGCCTCCTGGGCA   (SEQ ID NO:17)

55352   TAGTAGCTCCAGGCCCCTGTGAGTGAGGTCAGATCAGTTTTGATTCCGGCACTGCTGGCA
ACATAGGAGGCGCTGTCACTGCTGGGCTCTGGACCCTGTGGCCTGGCCCCCTGGAACATC
TTCCCCGGGATCAGGGGTCCTTGGACAGGCTGTTGTAAGGCTCGTCTGGAAGCCACAGCC
CAGGTCTGGGCAACTGCCTGGTGCCCTCAGCTGGGAGGCCTCTCTGGCAGAGGCGGCGGC
GTGGGATGTCGTCCAGTGTCCACAGCAGCCTGAGGCGAGGCGTCCCCTTGCCCCGGCTCT
[A,G]
CAGCGCCATGGGCTCGGGGCCTGTCTGGCTTGCTCGCTCACCTGCCTTGTTCTGTTTGTT
TTGGCTGCTCTGCCTTGCCCTGCCCTGCCCTGCCCTGGCTGGCTAGCTGCCCCGCTCCGC
ACTGGGAATGGCAGCTCGGTGCCTGAAGGACGGAGCTCCCGGGACAGAACAGCCCCCTCT
GCAGGCATGCAGCCCCAGCCTTCTCTCTGCTCCTCAGCCAGTAAGTGTGAGGGAGGCACA
TTCTGGCTTCCGTCTCCCTGGCTCGTCCTGAAGCCCCTCAGGGACCCCCACCACAGCTGT   (SEQ ID NO:18)

55914   CTCGTCCTGAAGCCCCTCAGGGACCCCCACCACAGCTGTCAGTCCCACCCACCTGCCCGT
GGTAGTAAGCTCTGGGAGCATGGCCTCTGCTGGGGGTGGGGGGTAGACTCGGAGGTGCTGT
TGAGACCAGGCAGGGGCCCCTGAGTCTCGGGGCCCAAAGAAATATGAGAAGTGTGGGTGGA
AAAACATGGCCTGGGATGAGGGGAGTAGAAAGCCCCCAGGATGTGCAGTGGGCCTTGCCT
CAGCGCTGAGCCAGGAAGAAGGGCAGAGTCGGAAGTCAGGTCTGTGGGGGTGGGAGTGGG
[A,G]
TGATGGGGAAATCGTGACAGCGAGGAACTGTGTTGGGGATGTAGTGCTTCCTGAGTCTCA
GCATAACAGTATTAAGAGCATGGGGTCAGAGGCAAGATAGATCTGAGTTTAAATCCCAGC
TACACTGCCTTCAAGAGTGTGAAGTTTAACCTCCCAGAGCTGCAGGTTCCTTATCTGTAA
TGTGGAAATAAAATGGCACGCACCTCAGAGCCTTGTTAGATAAAAGACAAGGCAGTAGGA
AGTCTTGATACGGTGCCTCGATGGGTTATCAGTAGCTCATCCTCATATTTCTAGTTACGT   (SEQ ID NO:19)

56633   TGGGGTTGGAGAGGGTGTGTGTGTTGTGGGTGCACACCTGCCTGCTGCTTTTGGAAGCCG
ATCGAACTCCTTGCTTCCCTTAACCTGCTGCTTGCTCACCTGGAGCTGTGGCCTAGCGGG
GCTGACGGCTGTGGGGCCCCCTCCTGGATGTGCCTTTGGCTGGCGCTGCCCTGTCCCAACT
GTGCTGCTTGGCTGTGCTGGCCCGGCTGGGCCGTGGTGGTGCTGTTCTAACGCTTGCAGT
TGTCTTGCAGCCTTTTGCTCCTGTGAGGAAAGGGTTGTGGCCTGGCCCCGCCCAGGGCTC
[G,A]
GGTTAGGATGAGCCCAAGCTCAACCCAAGCTCTCCCTTACCCTGGTGGCAGCCCCTGCTG
GTAGTGGCATTCCCTATAAGAGAAGCCCATGCCGGCAGGACATCACCAGCTGTCCCTTGG
CTTTGGATGGGTTGGGGAGGAGGCCTCTGGAGGGCACCACCTCTGCCTGCCTGTCAGTCT
GAGCCCTGTCTGGTTTTCCTGAGGAACACGTCCTGGCAATGAGAGCTGGTGTGAAATGTG
CAGCTTTCCCAAGCCTCGAGAGGTAAATGGAGCAGCCTCTCTGGTACAGGCTGTCCCAAG   (SEQ ID NO:20)

FIGURE 3Y